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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                              Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Title:
Perfect score:
                                                                                                                                                                                                                                                                                  Database :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Searched:
   SPTREMBL_21:*

1: sp_archea:*
2: sp_budeteria:
3: sp_fungi:*
4: sp_human:*
5: sp_invertebi:
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle
9: sp_plant:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebir
14: sp_unclass:
15: sp_urclass:
16: sp_bacteria:
17: sp_archeap:
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                               671580 seqs, 206047115 residues
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99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GenCore version 5.1.3 Compugen Ltd.
sp_vertebrate:*
sp_unclassified:*
sp_rvirus:*
sp_bacteriap:*
sp_archeap:*
                                                                              sp_plant:*
sp_rodent:*
sp_virus:*
                                                                                                                                                                                                                                              sp_archea:*
sp_bacteria:*
                                                                                                                                                    sp_organelle:*
                                                                                                                                                                                 sp_mammal:*
                                                                                                                                                                                                  sp_invertebrate: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

16	15	14	13	12	11	10	9	· co	7	o	U	4	ω	N		Result
47.5	48	49	49	49	50	50	50	50	50	51	51	51	52	99	99	Score
48.0	48.5	49.5	49.5	49.5	50.5	50.5	50.5	50.5	50.5	51.5	51.5	51.5	52.5	100.0	100.0	Query Match
273	466	1286	1160	842	847	720	502	462	449	700	700	700	406	285	284	Query Match Length
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057749	000096	P90936	P90935	Q9U3A8	Q9ADT8	Q9ER56	Q9ER55	Q9ER54	Q9ER53	Q9GLG1	Q8WU26	09нвв1	Q43509	Q9H812	Q63759	ID
057749 pyrococcus	000096 talaromyces	p90936 caenorhabdi	P90935 caenorhabdi	Q9u3a8 caenorhabdi	Q9adt8 salmonella	mus		Q9er54 mus musculu	ū	Q9glg1 macaca fasc	Q8wu26 homo sapien	Q9hbbl homo sapien	Q43509 lycopersico	Q9h812 homo sapien	Q63759 rattus norv	Description

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17
44	44	44	44	44.5		44.5	44.5	44.5		44.5	45	45	45	45	45	45.5	46	46	46	46	47	47	47	47	47	47	47	47
44.4	44.4	44.4	44.4	44.9	44.9	44.9	44.9	44.9	44.9	44.9	-	45.5		5					•	46.5	47.5	47.5	47.5	47.5	47.5	47.5	47.5	47.5
255	191	175	139	421	421	177	162	161	145	143	1227	724	551	385	344	739	703	549	381	327	703	566	486	456	301	245	245	186
10	2	16	10	16	16	17	16	N	2	N	16	13	N	10		2	•	17	11	16	11	ა	10	10	տ	16	16	N
Q8VYH9	Q8RSL4	Q98E68	Q9FK86	Q8YA00	Q92ES2	Q9YAM1	Q98P38	Q55215	Q54808	Q54526	Q9EWF3	Q8UW96	Q9RH54	023955	066257	087381	Q91VA3	Q8TWI2	62nt60	Q9I0M9	Q64698	016200	Q9FKQ1	Q9LX95	Q9GYC3	Q9Z4S4	Q8Z6K4	Q9F7D5
Q8vyh9 vernicia fo	Q8rs14 uncultured		Q9fk86 arabidopsis	Q8ya00 listeria mo		Q9yaml aeropyrum p	æ	Q55215 streptomyce	Q54808 streptomyce	co	Q9ewf3 streptomyce	Q8uw96 xenopus lae	Q9rh54 pantoea agg	023955 gossypium h		087381 haemophilus		Q8twi2 methanopyru	Q91uz9 mus musculu	Q910m9 pseudomonas	Q64698 rattus norv	O16200 caenorhabdi		Q91x95 arabidopsis	-	Q9z4s4 salmonella	Q8z6k4 salmonella	Q9f7d5 salmonella

ALIGNMENTS

Qy	X ¤ ⊙	SO	DR S	D D	R RA	RC	R R	, R	ŔŢ	RA	RX	RC :	R :	R (2 8	8	SO	GN	DE	J C	Di	DT	AC	ID	RESULT
1 PEWPSYLGYEKLGPYY 16	Query Match 100.0%; Score 99; DB 11; Length 284; Best Local Similarity 100.0%; Pred. No. 2.2e-07; Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Hydrolase. SEQUENCE 284 AA; 32557 MW; 8fb4448CCf0EfE83 CRC64;	Pfam; PF03370; CBM_21; 1.		Submitted (OCT-1998) to the EMBI/GenBank/DDBT databases	STRAIN-SPRAGUE DAWLEY;	SEOUENCE FROM N.A.	FEBS Lett. 375:294-298(1995).	(GL)-subunit of protein phosphatase-1.";	Doherty M.J., Moorhead G., Morrice N., Cohen P., Cohen P.T.;	MEDLINE~96085228; PubMed~7498521;	STRAIN-SPRAGUE DAWLEY;	SECUTENCE FROM N.A.	101_103.107.101.107	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus. NCRT TayTD=10116:	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Rattus norvegicus (Rat).	PPPIR4.	subunit (EC 3.1.3.16).	OL-JUN-2002 (TERMSLIEL 21, Last annotation update)	(TrEMBLrel. 10,	01-NOV-1996 (TrEMBLrel. 01, Created)	~~	Q63759 PRELIMINARY; PRT; 284 AA.	ILT 1

Db

269

PEWPSYLGYEKLGPYY

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Best Local S
Matches 16
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Q43509;
Q1-NOV-1996 (TrEMBLrel. 01, Create
01-NOV-1996 (TrEMBLrel. 01, Last s
G1-MAR-2002 (TrEMBLrel. 20, Last a
G-box binding protein (Fragment).
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Q9H812;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y., Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H., Wagatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara P. Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S. Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K., Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., Ninomiya K., Iwayanagi T., "NEDO human cDNA sequencing project.";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
CDNA FLJ14005 fis, clone Y79AA1002361, moderately similar to Rattus
                                                                             -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMIL
-!- SIMILARITY: BELONGS TO THE BZIP FAMILY.
EMBL; X74943; CAASZ897.1; -.
TRANSFAC: T02671; -.
InterPro; IPR004827; TF_bZIP.
Pfam; PF007170; bZIP; 1.
SMART; SM00338; BRLZ; 1.
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                                                                                                                                                                                                                                                                  "Novel Conserved sequence motifs in plant impications for interactive domains."; Nucleic Acids Res. 22:470-478(1994).
                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=CV. VENT LA 1221; TISSUE=3-8MM FRUIT;
MEDLINE=94173701; PubMed=8127687;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lycopersicon esculentum (Tomato).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Spermatophyta; Magnoliophyta; eudicotyledons; Solanales; 
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                              DNA-binding; Nuclear
                                                          PROSITE; PS00036; BZIP_BASIC;
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16; Conserv
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        protein.
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01, Last sequence update)
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Pred. No. 2.2
D; Mismatches
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RESULT 4
Q9HBB1
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RESULT RESULT OR WUZGE AC OR EN CONTROL OR MACO OR EN CONTROL OR MACO 
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Ol-JUN-2002 (TremBLrel. 21, Last
Hypothetical 80.0 kDa protein.
Homo sapiens (Human).
Eukaryota; Merayon
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InterPro; IPR001300; Protease_C2.
InterPro; IPR001300; Protease_C2.
InterPro; IPR000169; Shprot_acsite.
Pfam; PP01067; Calpain_III; 1.
Pfam; PP00036; efhand; 3.
Pfam; PP00648; Peptidase_C2; 1.
PRINTS; PR00704; CALPAIN.
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Q8WU26;
Q1-MAR-2002
Q1-MAR-2002
Q1-JUN-2002
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01-MAR-2001 (TrEMBLrel. 16,
01-MAR-2001 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
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                                                                                                                                Mammalia; Eutheria; NCBI_TaxID=9606;
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PROSITE; PS00139; THIOL_PROTEASE_CYS; 1.
SEQUENCE 700 AA; 79934 MW; DD304C603DEAC04C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART; SM00230; CysPc; 1.
SMART; SM00054; EFh; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Biochem. Biophys. Res. CommemBiochem. Biophys. Res. CommemBL; AF261089; AAF99682.1; HSSP; P04574; 1ALV.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae
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                       Submitted
                                         Strausberg R.;
                                                                   TISSUE=PANCREAS;
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                                                                                      SEQUENCE FROM N.A.
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cted (Jan-2002) to the
BC021303; AAH21303.1;
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9; Conser
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46.7%;
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                       EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                Last sequence update)
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Pred. No. 5.
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Pred. No.
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                                                                                                                                                         Craniata; Vo
Catarrhini;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hominidae;
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RESULT
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Q9GLG1
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                                                                                                                                                                                                                                                                                         R InterPro; IPR002048; EF-hand.
R InterPro; IPR001300; Protease_C2.
R InterPro; IPR001300; Protease_C2.
R InterPro; IPR000169; SHprot_acsite.
R Pfam; PF01067; Calpain_II; 1.
R Pfam; PF000548; Peptidase_C2; 1.
yR Pfam; PF000548; Peptidase_C2; 1.
yR PRINTS; PR00704; CALPAIN.
yR SMART; SM000230; Cyspc; 1.
yR SMART; SM00230; Cyspc; 1.
yR SMART; SM000230; Cyspc; 1.
yR SMART; SM00054; EFh; 3.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_I.
pROSITE; PS00139; THIOL_PROTEASE_CYS; 1.
scooleance 700 AA; 80026 MM; DCEE16214F05057C CRC64;
                                                                                                                                                                                                                                   Query Match
Best Local S
Matches 9
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Q9GLG1;
01-MAR-2001 (TrEMBLrel. 10
01-MAR-2001 (TrEMBLrel. 11
01-JUN-2002 (TrEMBLrel. 2
   Q9ER53;
Q9ER53;
01-MAR-2001
01-MAR-2001
01-JUN-2002
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SMART; SM00230; CYSPC; 1.

PROSITE; PS00018; EF_HAND; UNKNOWN_2.

PROSITE; PS00139; THIOL_PROTEASE_CYS; UNKNOWN_1.

Hypothetical protein.

SEQUENCE 700 AA; 80009 MW; 8D105821A4374FB2
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InterPro; IPR001300; Protease_C2.
InterPro; IPR000169; SHprot_acsite.
Pfam; PF01067; Calpain_III; 1.
Pfam; PF00036; efhand; 3.
Pfam; PF00648; Peptidase_C2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nakajima T., Fukiage C., Azuma M., Shearer T.R.;
"Calpain isoforms in the eye of monkey.";
"Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cercopithecinae: Macaca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Calpain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-RETINA;
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9; Conserv
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9; Conserv
   (TrEMBLrel. (TrEMBLrel.
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Pred. No.
                                                                                                                                                                                                                                                    Score 51; DB
Pred. No. 14;
                                                                           PRT;
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Q9ER54
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                    PAGPDALGYDKLGP
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Query Match
Best Local Similarity
Matches 9; Conserv
                                                             Query Match
Best Local
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Q9ER54;
01-MAR-2001
01-MAR-2001
01-JUN-2002
Calpain 12.
                                                                                                                  MGD; MGI:1891369; Capn12.
InterPro; IPR001300; Protease_C2.
InterPro; IPR00169; SHprot_acsite.
InterPro; IPR00169; SHprot_acsite.
Pfam; PF01067; Calpain_III; 1.
Pfam; PF00648; Peptidase_C2; 1.
PRINTS; PR00704; CALPAIN.
SMART; SM00230; CysPc; 1.
PROSITE; PS00139; THIOL_PROTEASE_CYS; 1.
PROSITE; PS00139; THIOL_PROTEASE_CYS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro: IPR001300; Protease_C2.
InterPro: IPR00169; SHprot_acsite.
Pfam; PF00648; Peptidase_C2; 1.
PRINTS; PR00704; CALPAIN.
SMART; SM00230; CysFc; 1.
PROSITE; PS00139; THIOL_PROTEASE_CYS; 1.
PROSITE; PS00139; THIOL_PROTEASE_CYS; 1.
                                                                                                                                                                                                                                                                                                                                                           Dear T.N., Meier N.T., Boehm T.;
"Gene structure, chromosomal localization and expression pattern Capn12, a new member of the calpain large subunit gene family.";
                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDLINE=20422668; PubMed=10964513; Dear T.N., Meier N.T., Boehm T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Capn12, a new member of the calpain Genomics 68:152-160(2000).

EMBL; AJ289243; CAC10070.1; -.
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Dear T.N., Meler N.T., Boehm T.;
"Gene structure, chromosomal localization and expression pattern
"Gene structure, chromosomal large subunit gene family.";
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CAPN12 OR CAPN12.
                                                                                                                                                                                                                                                                                                          MEROPS;
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1 PEWPSYLGYEKLGP 14
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                                        Similarity 64.: 9; Conservative
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l (TrEMBLrel. 16,
2 (TrEMBLrel. 21,
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                                                           50.5%;
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                                        Score 50; DB pred. No. 13; 1; Mismatches
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Last annotation update)
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                                                                            Length 462;
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Q9ER55;
01-MAR-2001
01-MAR-2001
                                      MGD; MGI:1891369; Capn12.
InterPro; IPR002048; EF-hand.
InterPro; IPR001300; Portease_C2.
InterPro; IPR00169; SHprot_acsite.
Pfam; PF01067; Calpain_III; 1.
Pfam; PF00648; Peptidase_C2; 1.
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SMART; SM00230; CysPc; 1.
PROSITE; PS00139; THTOL_PROTEASE_CYS; 1.
SEQUENCE 502 AA; 55874 MW; 816AC59F92226C3C CRC64;
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InterPro; IPR001300; Protease_C2.
InterPro; IPR00169; SPprot_acsite
Pfam; PF01067; Calpain_III; 1.
Pfam; PF00648; Peptidase_C2; 1.
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
SMART; SM00230; CysPc;
                                                                                                                                                                         MEROPS; C02.017; -.
                                                                                                                                                                                                                      Genomics 68:152-160(2000).
EMBL; AJ289241; CAC10066.1;
                                                                                                                                                                                                                                                               Capn12, a new member of the calpain
                                                                                                                                                                                                                                                                                                          Dear T.N., Meier N.T.,
                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. MEDLINE=20422668; PubMed=10964513;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAPN12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Calpain 12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2001
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9ER56;
01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9ER56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Capn12, a new member of the calpain large subunit gene family."; Genomics 68:152-160(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. MEDLINE-20422668; PubMed-10964513; Dear T.N., Meier N.T., Boehm T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAPN12
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                        PRINTS;
                                                                                                                                                                                                                                               MEDLINE=20422000,
Dear T.N., Meier N.T., Boehm T.;
"Gene structure, chromosomal localization and expression
"Gene structure of the calpain large subunit gene fi
                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                       Mammalia;
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                                                                                                                                                                                                                                                                                                                                                                                                                  musculus (Mouse).
aryota; Metazoa; Chordata;
malia; Eutheria; Rodentia;
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                        PR00704;
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Sciurognathi;
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Best Local
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Q9U3A8;
01-MAY-2000
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Boyd D., Peters G.A., Cloeckaert A., Boumedine K.S.,
Chaslus-Dancla E., Imberechts H., Mulvey M.R.;
"Complete Nucleotide Sequence of a 43-Kilobase Genomic Island
Associated with the Multidrug Resistance Region of Salmonella enterica
Serovar Typhimurium DT104 and Its Identification in Phage Type DT120
and Serovar Agona.";
J. Bacteriol. 183:5725-5732(2001).
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PROSITE;
SEQUENCE
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01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Putative subtilisin proteinase-like protein.
                                                                                                  Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditidae; Peloderinae; Caenorhabditis. NCBI_TaxID=6239;
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EMBL; AF261825; AAK02042.1; -.
InterPro; IPR000209; Peptidase_S8.
                      SEQUENCE FROM N.A. MEDLINE=99069613;
                                                                                                                                     Caenorhabditis elegans
                                                                                                                                                 M04C9.6C protein.
M04C9.6C.
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                                                         Submitted
                                                                               SEQUENCE
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Genome sequence of the nematode C.elegans: A platform
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9; Conserv
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PS00139; T
720 AA;
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; 95237 MW; 8E8D2843C2E21B93 CRC64;
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THIOL_PROTEASE_CYS;
80588 MW; 37C07BD
                       PubMed=9851916;
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Pred. No.
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RESULT 14
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Caeno
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RA Burto
RL Submi
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RP SEQUE
RA TONE;
RY "Genoe
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Matches 6
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Best Local (
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Science 282:2012-2018(1998).
EMBL; 283731; CADB6024.1; -.
InterPro; IPR000357; HEAT_repeat.
Pfam; PF02985; HEAT; 7
PROSITE; PS50077; HEAT_REPEAT; 3
SEQUENCE 1160 AA; 128667 MW; 4E
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Science 282:2012-2018(1998).
EMBL; E33731; CAB54273.1; -.
InterPro; IPR000357; HEAT_repeat.
Pfam; PF02985; HEAT; 4.
PROSITE; PS50077; HEAT_REPEAT; 2.
SEQUENCE 842 AA; 92993 MW; CDAB45787193F842 CRC64;
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Eukaryota; Metazoa; Nemat
Rhabditidae; Peloderinae;
   Submitted
                      Burton
                                      SEQUENCE FROM N.A.
                                                                                           Caenorhabditis elegans.
Eukaryota; Metazoa; Nemat
Rhabditidae; Peloderinae;
                                                                                                                                                  M04C9.6a protein.
M04C9.6A.
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01-MAY-1997 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
M04C9.6b protein.
                                                                          NCBI_TaxID=6239;
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rinae; Caenorhabditis.
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Pred. No.
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RESULT 15
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Search completed: January 13, 2003, Job time: 30 secs
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""" Best B; Conserva
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000096;
01-JUL-1997
01-JUL-1997
01-MAR-2002
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Pfam; PF00328; acid_phosphat; 1.
PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; UNKNOWN_1.
Hydrolase.
                                                                                                                                                                                                                                                                                                                                                                                                                  fungus Talaromyces thermophilus.";
Biochim. Biophys. Acta 1333:217-223(1997).
EMBL; U59802; AAB96873.1; -.
HSSP; P34752; 11HP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     investigating biology.";
Science 282:2012-2018(1998).
EMBL; Z83731; CABB6025.1; -.
InterPro; IDR000357; HEAT_repeat.
Pfam; PF02985; HEAT; 7.
PROSITE: PS50077; HEAT_REPEAT; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pasamontes L., Haiker van Loon A.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. MEDLINE=98007872; PubMed=9349716;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Fungi; Ascomycota; Pezizomyco
Eurotiales; Trichocomaceae; Talaromyces
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SEQUENCE FROM N.A.
MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=28565;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Talaromyces thermophilus
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                                                                                               285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cloning of the phytases from Emericella
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Last annotation update)
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Pred. No.
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Pred. No.
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Match Length
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 SwissProt_40:*
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 DB
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                              CANB_HUMAN
CAN1_HUMAN
SUF1_XENLA
PLSB_XYLFA
NARG_BACSU
NARZ_ECOLI
                 SUF1_HUMAN
BXA1_CLOBO
                                                                     SAHH_STRAA
BXA2_CLOBO
PSAB_MAIZE
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      P08830
P19666
Q9cun6
Q9umq6
P07384
Q9pun7
Q9pun7
P10845
Q9pej7
P42175
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Q63014
P26799
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Q92178
Q9hau4
P15773
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Q07384
Q936d6
Q45894
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tetrahymena
mus musculu
           homo sapien
clostridium
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sulfolobus
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clostridium
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saccharomyc
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				Q9m1s8 arabidopsis							P36290 c genome po	P09152 escherichia

ALIGNMENTS

MOUSE

CAN2_MOUSE STANDARD; PRT; 700 AA.

008529; 035518; 054843;
01-NOV-1997 (Rel. 35, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
Calpain 2, large [catalytic] subunit precursor (EC 3.4.22.17)
(Calcium-activated neutral proteinase) (CANP) (M-type) (M-calpain)
(Millimolar-calpain) (80 kDa M-calpain subunit) (CALP80). Mus musculus (Mouse).
Mus musculus (Mouse).
***Total Metazoa; Chordata; formula; Metazoa; Rodentia; MEDLINE-97480729; PubMed-9339374;
Dear N., Matena K., Vingron M., Boehm T.;
"A new subfamily of vertebrate calpains lacking a calmodulin-like domain: implications for calpain regulation and evolution.";
Genomics 45:175-184(1997). Eukaryota; Metazoa; Mammalia; Eutheria; NCBI_TaxID=10090; STRAIN-BALB/C SEQUENCE FROM N.A. Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus

Ozaki STRAIN-BALB/c; SEQUENCE FROM N.A.

Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.

TISSUE-CNS; SEQUENCE FROM N.A.

Glass J.D., Nash N.R., Dry I., Culver D., Wesselingh S.;
"Cloning of m-calpain from mouse nervous system.";
Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Calcium-regulated non-lysosomal thiol-protease which catalyze limited proteolysis of substrates involved in cytoskeletal remodelling and signal tranduction (By similarity).
-!- CAPALYTIC ACTIVITY: Preferential cleavage: Tyr-|-Xaa, Met-|-Xaa or Arg-|-Xaa with Leu or Val as the P2 residue.
-!- COPACTOR: Binds 3 calcium ions.
-!- ENZYME REGULATION: Activated by 200-1000 micromolar concentrations

-!- ENZYME REGULATION: Activated by 200-1000 micromolar concentrations of calcium and inhibited by calpastatin.
 -!- SUBUNIT: Heterodimer of a large (catalytic) and a small

(regulatory) subunit.
-!- SUBCELLULAR LOCATION: Cytoplasmic; membrane upon Ca++ binding. SIMILARITY: CONTAINS 5 EF HAND CALCIUM-BINDING DOMAINS. SIMILARITY: BELONGS TO PEPTIDASE FAMILY C2. Translocates to the plasma

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RESULT 2
CAN2_RAT
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Best Local S
Matches 10
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EMBL; D38117; BA
EMBL; AF015038;
HSSP; Q07009; 1D
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CA_BIND
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                                                                                                                         CAN2_RAT STANDARD; PRT; 700 AA.

Q07009;
Q1-JUN-1994 (Rel. 29, Created)
Q1-JUN-1994 (Rel. 29, Last sequence update)
Q1-JUN-1994 (Rel. 29, Last sequence update)
S-JUN-2002 (Rel. 41, Last annotation update)
Calpain 2, large [catalytic] subunit precursor (EC 3.4.22.17)
(Calcium-activated neutral proteinase) (CANP) (M-type) (M-calpain)
                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00639; THIOL_PROTEASE_HIS; FALSE_NEG.
PROSITE; PS00640; THIOL_PROTEASE_HIS; FALSE_NEG.
Hydrolase; Thiol protease; Calcium-binding; Repeat; Multigene fam
PROPEP
1 19 ANCHORS TO THE SMALL SUBUNIT (POTENT
PROPEP
1 19 CALPAIN 2, LARGE [CATALYTIC] SUBUNIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pfam; PF00036; efhand; 3.
pfam; PF00648; Peptidase_C2; 1.
pfam; PF01067; Calpain_III; 1.
pRINTS; PR00704; CALPAIN.
proDom; PD000012; EF-hand; 1.
                                                                                                                                                                                                                                                                                                                 SEQUENCE
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InterPro; IPR001300; Protease_C2.
InterPro; IPR000169; SHprot_acsite.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEROPS; C02.002; -. MGD; MGI:88264; Capn2.
         MEDLINE=94032492; PubMed=8218419;
Deluca C.I., Davies P.L., Samis J.A., Elce of Medica Coning and bacterial expression II 80 kDa subunit.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
Biochim.
                                                                 Mammalia; Eutheria;
NCBI_TaxID=10116;
                                                                              Eukaryota;
Mammalia; E
                                                SEQUENCE FROM N.A.
                                                                                              Rattus norvegicus (Rat).
                                                                                                                    (Millimolar-calpain).
                                                                                                                                                                                                                                      52
                                                                                                                                                                                                                                                        1 PEWPSYLGYEKLGPY 15
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                                                                                                                                                                                                                                      PALPSSLGYKELGPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SM00230; CysPc;
SM00054; EFh; 2.
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PS00139;
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Biophys.
                                                                                      Metazoa;
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THIOL_PROTEASE_CYS;
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                                                                             Rodentia;
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66.7%;
1216:81-93(1993).
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A -> T (IN REF. 1).
A -> G (IN REF. 2).
A -> G (IN REF. 2).
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EF-HAND 2.
EF-HAND 3.
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DOMAIN IV.
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THIOL PROTEASE DOMAIN II.
DOMAIN III, C2-LIKE DOMAI
                                                                             Sciurognathi;
                                                                                      Craniata;
                                                                                                                                                                                                                                                                                                                 -> G (IN REF. 2)
-> G (IN REF. 1)
682146B290968316
                                                                                                                                                                                                                                                                                 DB
).7;
                                                                                       Vertebrata; Euteleostomi;
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                              C
                    of.
                                                                             Muridae;
                             'n
                                                                                                                                                                                                                                                                                                                                                                                    SITE
                                                                                                                                                                                                                                                                                              Length 700;
                     CDNA
                                                                                                                                                                                                                                                                                                                  CRC64;
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                      for
                                                                               Murinae;
                                                                                                                                                                                                                                                                                                                                                                                    (POTENTIAL).
                     rat calpain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (POTENTIAL)
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                                                                               Rattus
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Pfam; PF01067; Calpain_III; 1.

PRINTS; PR00704; CALPAIN.

PRODOM; PD000012; EF-hand; 1.

SMART; SM00230; CysPc; 1.

SMART; SM00230; CysPc; 1.

SMART; SM00054; EFh; 2.

PROSITE; PS000018; EF_HAND; 2.

PROSITE; PS000139; THIOL_PROTEASE_CYS; 1.

PROSITE; PS000640; THIOL_PROTEASE_ASN; FP
PROSITE; PS000640; THIOL_PROTEASE_ASN; FP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBO
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PARTIAL SEQUENCE.
MEDLINE=21240297; PubMed=11342050;
Moldoveanu T., Hosfield C.M., Jia Z., Elce
"Ca(2+)-induced structural changes in rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hosfield C.M., Elce J.S., Davies P.L., Jia Z., "Crystal structure of calpain reveals the structural Ca(2+)-dependent protease activity and a novel mode of the control of the case activity and a novel mode of the case activity activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEBS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no restr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mutagenesis."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arthur J.S., Gauthier S., Elce J.S., "Active site residues in m-calpain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Blochim.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=95361909; PubMed=7635186;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MUTAGENESIS OF CYS-105; HIS-262;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=21269273;
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                                                                                                                                                                                                                                                            Pfam;
                                                                                                                                                                                                                                                                                 Pfam;
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PDB; 1DF0; 21-JUN-00.
MEROPS; C02.002; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; L09120;
                                        Hydrolase;
                                                                                                                                                                                                                                                                                                          InterPro;
                                                                                                                                                                                                                                                                                                                            InterPro;
                                                                                                                                                                                                                                                                                                                                              InterPro;
                    D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Biol. Chem. 276:7404-7407(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arg-|-Xaa with Leu or Val as the P2 residue. CGFACTOR: Binds 3 calcium ions. ENZYME REGULATION: Activated by 200-1000 micromolar of calcium and inhibited by calpastatin. SUBUNIT: Heterodimer of a large (catalytic) and a sm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: Calcium-regulated non-lysosomal thiol-pro-
catalyze limited proteolysis of substrates involved
cytoskeletal remodelling and signal tranduction.
CATALYTIC ACTIVITY: Preferential cleavage: Tyr-|-Xa:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (regulatory) subunit.
SUBCELLULAR LOCATION: Cytoplasmic; Translocates
membrane upon Ca++ binding.
SIMILARITY: CONTAINS 5 EF-HAND CALCIUM-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: BELONGS TO PEPTIDASE FAMILY C2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  <u>-</u>
                                                                                                                                                                                                                                                                                   PF00036;
                                                                                                                                                                                                                                                               PF00648;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Biophys. Acta 1545:245-254(2001).
                                                                                                                                                                                                                                                                                                       IPR002048; EF-hand.
IPR001300; Protease_C2
IPR000169; SHprot_acsi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         368:397-400(1995).
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                                          Thiol
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                                                                                                                                                                                                                                                                                   efhand;
                                                                                                                                                                                                                                                            Peptidase_C2; 1.
                                          protease;
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19
                                                                                                                                                                                                                                                                                                     SHprot_acsite.
                                          Calcium-binding; Repeat; Multigene
    ANCHORS
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  TO THE SMALL SUBUNIT
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                                                               FALSE_NEG
                                                                                     FALSE_NEG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Davies P.L.;
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    (POTENTIAL)
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Best Local S
Matches
                                                                                                                                                                                    Eukaryota; Viridiplantae; Strep
Spermatophyta; Magnoliophyta; L
Triticeae; Triticum.
                                                                                                                                                                                                                                            P23922;
01-MAR-1992 (Rel. 21, C
01-MAR-1992 (Rel. 21, I
15-JUN-2002 (Rel. 41, I
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      "Developmental and tissue-specific regul
"Developmental and tissue-specific regul
wheat basic/leucline zipper protein HBP-1
Arabidopsis plants.";
                                     STRAIN=cv. Horoshirikomugi;
MEDLINE=96027929; PubMed=7476857;
                                                                   "A protein that binds to a cis-acting has a leucine zipper motif."; Science 245:965-967(1989).
                                                                                            Tabata T., Takase H.,
Nakayama T., Iwabuchi
                                                                                                                                   EMBO
                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE-91224097; PubMed-2026143;
Tabata T., Mikami K.,
"HBP-1a and HBP-1b: leucine zipper-
                                                                                                                                                                                                                                      Transcription
                                                                                                                                                                                                                                                                            WHEAT
HBPA_WHEAT
                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                      SEQUENCE
                                                                                                  MEDLINE-89368924; PubMed=2772648;
Tabata T., Takase H., Takayama S.,
                                                                                                                   SEQUENCE FROM N
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PALPSSLGFKELGPY
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9; Conserv
                                                                                                                                  10:1459-1467(1991).
                                                      FROM
 Genet.
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                                                      N.A.
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248:573-582(1995)
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Last annotation
HBP-la (Histone-s
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                                                                                                                                                                                                     Streptophyta; Er
yta; Liliopsida;
                                                                                                                                                zipper-type
                                                                                                                                                                                                                                     annotation update) (Histone-specific
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EF-HAND 1.
EF-HAND 3.
ANCESTRAL CALCIUM S
ANCESTRAL CALCIUM S
                                                                                                                                                                                                                                                                                                                                              Pred. No. 2./;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                        Score 52;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                               N->A:
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K->E:
H->A:
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DECREASE OF 85% OF T
DECREASE OF 20% OF T
LOSS OF ACTIVITY.
LOSS OF ACTIVITY.
DECREASE OF 95% OF T
DECREASE OF 10% OF T
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NO EFFECT
                                                                                                  Mikami K.,
              regulation HBP-1a(17)
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                                                                                                                                                                                                                                                                             349
                                                                                   element of wheat histone
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REASE OF 95% OF T
REASE OF 10% OF T
3BEEF5B90 CRC64;
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2.7;
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a; Poales; Poaceae;
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EASE OF 12% OF
             Shimura lation of la(17) in
                                                                                                                                                transcription
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                                                                                                                                                                                                                                     transcription
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                       Y.,
the
               transgenic
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                       gene
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                             Iwabuchi
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DT 01-AUG
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DE CALPAI
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Best Local S
Matches 7
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CAN2_HUMAN STANDAND,
P17655; Q16738;
O1-AUG-1990 (Rel. 15, Created)
O1-AUG-1990 (Rel. 15, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Calpain 2, large [catalytic] subunit precursor (EC 3.4...)
Calpain 2, large [catalytic] subunit precursor (EC 3.4...)
                                                                                                                                                                                                                                                                            Imajoh S.,
Suzuki K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TRANSFAC; T00354; -. TRANSFAC; T00937; -. InterPro: IPR004827; TF_bzIP.
                        dependent
J. Biol. (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR;
PIR;
HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X56781; CAA40101.1; -. EMBL; M28704; AAA34293.1; -. EMBL; D38111; BAA07289.1; -.
                                         transcription of a human dependent protease.";
                                                                             TISSUE-Lymph node:
MEDLINE-89197947; PubMed-2539381;
Hata A., Ohno S., Akita Y., Suzuki K.;
"Tandemly reiterated negative enhancer
                                                                                                                                                                                                            "Molecular cloning of the cDNA for high-Ca2+-requiring form of human C Biochemistry 27:8122-8128(1988).
                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE-89166474; PubMed-2852952;
Imajoh S., Acki K., Ohno S., Emori
                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transcription regulation; DNA-binding; Activator; Nuclear protein. DNA_BIND 254 273 BASIC MOTIF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00170; bZIP; 1. SMART; SM00338; BRLZ; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human)
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                                                                                                                                                                       SEQUENCE OF 1-79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         - FUNCTION: BIND TO THE H
GENE PROMOTERS.
- SUBUNIT: BINDS DNA AS /
- SUBCELLULAR LOCATION: N
- SIMILARITY: BELONGS TO
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S15346; S15346.
P03069; 2DGC.
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                                                                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Catarrhini; Hominidae;
                                                               enhancer-like for the large
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                                                                                                                                                                                                                                                                                                Kawasaki H.,
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of calcium
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InterPro; IPR00169; SHprot_acsite.
Pfam; PF00036; efhand; 3.
Pfam; PF000648; Peptidase_C2; 1.
Pfam; PF01067; Calpain_III; 1.
PRINTS; PR00704; CALPAIN.
ProDom; PD000012; EF-hand; 1.
                                                                             DOMAIN
CA_BIND
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CA_BIND
CA_BIND
DOMAIN
ACT_SITE
ACT_SITE
                       CONFLICT
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DOMAIN
    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00230; CysPc; 1.
SMART; SM00054; EFh; 2.
PROSITE; PS00018; EF_HAND; 2.
PROSITE; PS00139; THIOL_PROTEASE_CYS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genew; HGNC:1479; CAPN2. MIM; 114230; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M23254; AAA35645.1; -.
EMBL; J04700; AAA52760.1; -.
EMBL; A31218; A31218
PDB; 1KFU; 07-DEC-01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement (Some send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "The crystal structure of calcium-free human m-calpain suggests electrostatic switch mechanism for activation by calcium.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strobl S., Fernandez-Catalan
                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00639; PROSITE; PS00640;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Proc. Natl. Acad. Sci. U.S.A. 97:588-592(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Suzuki K., Bode W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=20105516;
                                                                ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                         Hydrolase;
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                                                                                                                                                                                                                                                                                                                                                                    D-structure.
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SUBCELLULAR LOCATION: Cytoplasmic; Translocates
membrane upon Ca++ binding.
SIMILARITY: CONTAINS 5 EF-HAND CALCIUM-BINDING
SIMILARITY: BELONGS TO PEPTIDASE FAMILY C2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: Calcium-regulated non-lysosomal thiol-protease which catalyze limited proteolysis of substrates involved in cytoskeletal remodelling and signal tranduction.

CATALYTIC ACTIVITY: Preferential cleavage: Tyr-|-Xaa, Met-|-Xaa Arg-|-Xaa with Leu or Val as the P2 residue.

COFACTOR: Binds 3 calcium ions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of calcium and inhibited by calpastatin SUBUNIT: Heterodimer of a large (catalyterofield)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ENZYME REGULATION: Activated by 200-1000 micromolar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SWISS-PROT entry is copyright. It is produced through a sen the Swiss Institute of Bioinformatics and the EMBI
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                         ernandez-Catalan C., Braun
Irie A., Sorimachi H., Bou
    AA;
                                                                                                                                                                                                                                                                                                                                                                                           protease;
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    MW.
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                                                                                                                                                                                                                                                                                                                                                                                       Calcium-binding;
                                       BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
S -> G (IN REF.
                                                                                                                                                               EF-HAND 1.
EF-HAND 2.
EF-HAND 3.
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                                                                                                                       ANCESTRAL CALCIUM ANCESTRAL CALCIUM
                                                                                                                                                                                                                         DOMAIN IV.
                                                                                                                                                                                                                                                                                                                            ANCHORS TO THE SMALL SUBUNIT CALPAIN 2, LARGE [CATALYTIC]
-> G (IN REF. 2).
R -> IE (IN REF. 2).
A944Dl3BC8465531 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (catalytic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                aun M., Huber R., Masumo
Bourenkow G., Bartunik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                     Repeat; Multigene family;
                                                                                                                       SITE
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                                                                                                                       (POTENTIAL).
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L outstation -
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Matches 9; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=86082358; PubMed=3000828;
Emori Y., Ohno S., Tobita M., Suzuki K.;
"Gene structure of calcium-dependent protease retains
organization of the calcium-binding protein gene.";
FEBS Lett. 194:249-252(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-JUL-1986 (Rel. 01, Createo)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                       muscle expresses four distinct calpains."; Biochim. Biophys. Acta 1261:381-393(1995).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                activated neutral proteinase) (CANP) (Mu/M-type). Gallus gallus (Chicken). Eukaryota, Metazoa, Chordata; Craniata; Vertebrata; Eutel Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
                                                                                                                                                                                                                                                                                                                                                                                    Sorimachi H.,
                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=95260862;
                                                                                                                                                                                                                                                                                                                                                                                                                CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-87279982; PubMed=3038855;
Minami Y., Emori Y., Kawasaki H., Suzuki K.;
"E-F hand structure-domain of calcium-activated
(CANP) can bind Ca2+ ions.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CALCIUM-BINDING DATA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 312:566-570(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                         "Identification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ohno S., Emori Y., Imajoh S., Kawasaki H., Kisaragi M., Evolutionary origin of a calcium-dependent protease by genes for a thiol protease and a calcium-binding protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     52
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                         membrane upon Ca++ binding (By similarity).
TISSUE SPECIFICITY: UBIQUITOUSLY EXPRESSED.
PTM: THE N-TERMINUS IS BLOCKED.
SIMILARITY: Contains 5 EF-hand calcium-binding cistumitarity: BELONGS TO PEPTIDASE FAMILY C2.
CAUTION: THIS PROTEIN WAS PREVIOUSLY THOUGHT TO HAS SINCE BEEN FOUND TO BE AN INTERMEDIATE FORM MU TYPES.
                                                                                                                                                                              FUNCTION: Calcium-regulated non-lysosomal thiol-protease which catalyze limited proteolysis of substrates involved in cytoskeletal remodelling and signal tranduction.

CATALYTIC ACTIVITY: Preferential cleavage: Tyr-[-xaa, Met-[-xaa, Met-]-xaa with Leu or Val as the P2 residue.

COFACTOR: Binds 3 calcium inos.

ENZYME REGULATION: Activated by micromolar concentrations of calcium and inhibited by calpastatin.

SUBUNIT: Heterodimer of large (catalytic) and a small (regulator)
                                                                                                                                                  subunit.
SUBCELLULAR LOCATION: Cytoplasmic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PAIPSALGFKELGPY
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                                                                                                                                                                                                                                                                                                                                                                                    Tsukahara
                                                                                                                                                                                                                                                                                                                                                                                                    PubMed=7742367;
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                                                                                                                                                                                                                                                                                                                                                    a third ubiquitous
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3.8;
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Matches 8
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DOMAIN
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Kawarabayasi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., Kosugi H., Hosoyama A., Fukui S., Sekine M., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Yoshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yamagishi A., Oshima T., Kikuchi H.;
                                                                       STRAIN-JCM 10545 / 7;
MEDLINE-21456156; PubMed-11572479;
                                                                                                                                                                                         15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Thermostable DNA ligase (EC 6.5.1.1) (Polydeo
                                                                                                                                                                                                                                          DNLI_SULTO Q976G4;
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DOMAIN
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PROSITE; PS00139; THIOL_PROTEASE_CYS; 1.

PROSITE; PS00639; THIOL_PROTEASE_HIS; FALSE_NEG.

PROSITE; PS00640; THIOL_PROTEASE_ASN; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PR00704; CALPAIN.
ProDom; PD000012; EF-hand; 1.
SMART; SM00230; Cyspe; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR002048; EF-hand.
InterPro; IPR001300; Protease_C2.
InterPro; IPR000169; SHprot_acsite.
Pfam; PF00036; efhand; 2.
Pfam; PF00648; Peptidase_C2; 1.
Pfam; PF0167; Calpain_III; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                          Sulfolobus
                                                                                                                                                                              synthase [ATP]).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; X01415; CAA25658.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or send an email to license@isb-sib.ch).
                                                                                              SEQUENCE FROM N.A.
                                                                                                                                               Archaea;
                                                                                                                     NCBI_TaxID=111955;
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P; Q07009;
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8; Conserv
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                                                                                                                                             Crenarchaeota;
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53.3%;
                                                                                                                                             Thermoprotei;
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                                                                                                                                                                                                                                                                                                                                                            Score 49; DB
Pred. No. 7.7;
4; Mismatches
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LINKER.
LOMAIN IV.
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EF-HAND 3.
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    (Polydeoxyribonucleotide

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Best Local S
Matches 7
                                                                                                                                                                                                                                                                                                                                                          LAIX., Shao H., Huang L.;
LAIX., Shao H., Huang L.;
"A thermophilic DNA ligase from Sulfolobus shibatae.";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: THIS PROTEIN SEALS DURING DNA REPLICATION, Depring that the process of the process 
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Q9P9K9;
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SEQUENCE
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DNA ROS. 8:123-140(2001).

-I- FUNCTION: THIS PROTEIN SEALS

PERCOMBINATION AND DNA REPAIR
                    This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entrepean Bioinformatics Institute. There are no restructe by non-profit institutions as long as its content modified and this statement is not removed. Usage by anomalized and this statement is not removed.
                                                                                                                                                                                                                                                                 SIMILARITY).
-i- CATALYTIC ACTIVITY: ATP + {deoxyribonucleotide}(N)
-i- CATALYTIC ACTIVITY: AMP + diphosphate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sulfolobus shipara.
Archaea; Crenarchaeota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00697; DNA_LIGASE_A1; 1.
PROSITE; PS00333; DNA_LIGASE_A2; 1.
PROSITE; PS50160; DNA_LIGASE_A3; 1.
DNA repair; DNA replication; DNA recombination; Cell division; Ligase; DNA repair; DNA reproteome.
DNA repair; DNA replication; DNA recombination; Cell division; Ligase; DNA repair; DNA reproteome.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF01068; DNA_ligase; 1.
TIGRFAMS; TIGR00574; dnll; 1.
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-!- CATALYTIC ACTIVITY: ATP +
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15-JUN-2002
                                                                                                                                                                                                                        -!- SIMILARITY: BELONGS TO THE ATP-DEPENDENT DNA LIGASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=2286;
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{deoxyribonucleotide}(N+M).
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eon, Sulfolobus tokodaii strain7.";
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l (Rel. 40, Las
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11gase (EC 6.5.1.1) (Polydeoxyribonucleotide
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Pred. No.
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AMP + diphosphate +
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
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STRAIN-RCC 35092 / DSM 1617 / P2;
MEDLINE-21332296; PubMed=11427726;
She Q., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.
Awayez M.J., Chan-Weiher C.C.-Y., Clausen I.G., Curtis B.A.,
De Moors A., Erauso G., Fletcher C., Gordon P.M.K.,
Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., F
Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., F
Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstru
Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T.,
Garrett R.A., Ragan M.A., Sensen C.W., Van der Oost J.;
                PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    i5-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last sequence update)
Thermostable DNA ligase (EC 6.5.1.1) (Polydeoxyribonucleotide synthase [ATP]).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE;
                                                                                                                                                                                                                                                                                                     Garrett R.A., Ragan M.A., Sensen C.W., Van der Oost J.; "The complete genome of the crenarchaeon Sulfolobus solfataricus Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SULSO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam;
                                                                                                        entities requires a or send an email to
                                                                                                                                use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNLI_SULSO Q980T8;
                                        Pfam; PF01068; DNA_ligase; TIGRFAMS; TIGR00574; dnll;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sulfolobus solfataricus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL;
                                                                                                                                                           the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=2287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Archaea; Crenarchaeota;
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                                                                   nterPro;
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                                                                                                                                                                                                            (deoxyribonucleotide)(N+M). SIMILARITY: BELONGS TO THE ATP-DEPENDENT DNA LIGASE FAMILY.
                                                                                                                                                                                                                                       CATALYTIC ACTIVITY: ATP + {deoxyribonucleotide}(N) {deoxyribonucleotide}(M) = AMP + diphosphate +
                                                                                                                                                                                                                                                                              FUNCTION: THIS PROTEIN SEALS DURING DNA REPLICATION, RECOMBINATION AND DNA REPAIR NICKS IN DOUBLE-STRANDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OR SSO0189
                                                                                                                                                                                                                                                                  SIMILARITY)
                                                                                                                                                                      SWISS-PROT entry is copyright. It is producen the Swiss Institute of Bioinformatics
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                                                                              AE006656; AAK40535.1; -
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PS00697; DNA_LIGASE_A1; 1.
PS00333; DNA_LIGASE_A2; 1.
PS50160; DNA_LIGASE_A3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PS00697; DNA_LIGASE_A1; 1.
PS00333; DNA_LIGASE_A2; 1.
PS50160; DNA_LIGASE_A3; 1.
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                                                                  IPR000977; DNA_ligase.
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67646 MW;
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Phosphorylation.

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ACT_SITE
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MOD_RES
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                                                                                                                                                                                                                                                                                                                                               InterPro; IPR002290; Ser_thr_p
Pfam; PF00069; pkinase; 1.
ProDom; PD000001; Euk_pkinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no rest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           J. Biol. Chem. 268:21044-21052(1993).
-!- FUNCTION: MAY BE INVOLVED IN SOME STAGE-SPECIFIC ROLE IN PROMASTIGOTE CELL CYCLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA repair; DNA replication; ATP-binding; Complete proteon
                                                                                                                                                                                                                             PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SUBUNIT: FORMS A STABLE BUT NON-COVALENT COMPLEX WITH A REGULATORY SUBUNIT AND WITH A CYCLIN (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- ENZYME REGULATION: PHOSPHORYLATION AT THE ENZYME, WHILE PHOSPHORYLATION AT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "A novel CDC2-related protein kinase from I LmmCRK1, is post-translationally regulated J. Biol. Chem. 268:21044-21052(1993).
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PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
                                                                                                                                                                                                                                                                                                                     SMART; SM00220;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DEVELOPMENTAL STAGE: EXPRESSED IN ALL LIFE CYCLE STAGES, PROMASTIGOTE, METACYCLIC AND AMASTIGOTE FORMS BUT IS FOR IN THE ACTIVE FORM ONLY IN THE PROMASTIGOTE STAGE. SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KIN
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30, Last sequence 38, Last annotations.
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63.6%;
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se; 1.
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kinase 2 homolog CRK1 (
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                                PROTEIN KINASE.
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Trypanosomatidae; Leishmania.
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RESULT 10
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MOD_RES
SEQUENCE
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Relaischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F., Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weldman J.F., Phillips C.A., Spriggs T., Hebback B., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                                 use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for contribes requires a license according to the statement of the statement
                                                                     EMBL; U32764; AAC22477.1;
EMBL; X65934; CAA46732.1;
PIR; S21448; S21448.
PIR; S27989; S27989.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Maskell D.J., Szabo M.J., Deadman M.E., Moxon E.R.; "The gal locus from Haemophilus influenzae: cloning, the use of gal mutants to study lipopolysaccharide."; Mol. Microbiol. 6:3051-3063(1992).
                                                                                                                                                                                           entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=RM 7004 / Serotype B;
MEDLINE=93125127; PubMed=1282642;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Science 269:496-512(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=727;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Aldose 1-epimerase (EC GALM OR MRO OR HI0818.
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                                                   TIGR; HI0818;
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15-JUN-2002 (Rel. 41,
                             InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Whole-genome random sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        251 PEWSNVLGSVPGYEKLG 267
                                                                                                                                                                                                                                                                                                                                                                               PATHWAY: Hexose metabolism.
SUBCELLULAR LOCATION: Cytoplasmic
SIMILARITY: BELONGS TO THE ALDOSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                 is active on D-glucose, L-arabinose, D-xylose, D-galimaltose and lactose (By similarity).

CATALYTIC ACTIVITY: Alpha-D-glucose - beta-D-glucose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: Mutarotase converts alpha-aldose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PEWPSYL ---
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IPR001823; Ald1_epimerase
1263; Aldose_epim; 1.
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301
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160
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Pred. No.
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PHOSPHORYLATION (BY CAK) (BY SIMILARITY).
58EB39D006D88461 CRC64;
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(Mutarotase).
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Nahon ..... Sala-Trepat J.M.;
Sala-Trepat J.M.;
"The rat alpha-fetoprotein and albumin yunamed comparison of the sequence organization and comparison of the sequence organization of the sequence organization and comparison of the sequence organization and comparison of the sequence of 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Rat alpha 1-fetoprotein messenger RNA: 5'-end sequence glucocorticoid-suppressed liver transcription in an impr run-off assay.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Isomerase;
ACT_SITE
VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Jagodzinski L.L., Sargent T.D., Yang M., "Sequence homology between RNAs encoding rat serum albumin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VARIANT
VARIANT
                                                                                                                                                                                                     MEDLINE=87146445; pubMed=2434929;
Chevrette M., Guertin M., Turcotte B., Belanger L.,
"The rat alpha 1-fetoprotein gene: characterization
5'-flanking region and tandem organization with the
                                                                                                          MEDLINE-87308273; PubMed-2442163; Nahon J.L., Danan J.L., Poiret M.,
                                                                                                                                                                                                                                                                                                                                           DNA
                                                                                                                                                                                                                                                                                                                                                         MEDLINE=92119318; PubMed=1722723; Buzard G.S., Locker J.; "The transcription control region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=Sprague-Dawley;
MEDLINE=85215621; PubMed=2582363;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-JUL-1986 (Rel.
21-JUL-1986 (Rel.
15-JUN-2002 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FETA_RAT
P02773; Q63032;
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                                                                                                                                                                                         Nucleic
                                                                                                                                                                                                                                                                                      SEQUENCE
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                                                                                                                                                                                                                                                                                                                        Seq. 1:33-48(1990)
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ALDOSE_1_EPIMERASE;
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N -> K (IN STRAIN RM 7004)
N -> K (IN STRAIN RM 7004)
4ECAE4FB8C498C7A CRC64;
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Let nomology between rat alphatine COOH-terminal regions.";

U. Biol. Chem. 255,8046-8049(1980).

CC -!- FUNCTION: Binds estrogens, fatty acids and met CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- TISSUE SPECIFICITY: Plasma.

CC -!- TISSUE SPECIFICITY: Plasma.

CC -!- SIMILARITY: Proceedings of the company of the comp
RESULT 12
CAN2_CHICK
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Best Local
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PROSITE; PS00212; ALBUMII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PR00802; SERUMALBUMIN. ProDom; PD002486; Serum_albumi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP; P02768; 1E7B.
InterPro; IPR000264; Serum_albumin.
Pfam; PF00273; transport_prot; 3.
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albumin at the COOH-terminal regions.";
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                                                                                                           YOKLGPYY 428
                                                                                                                                                             YEKLGPYY 16
                                                                                                                                                                                                                 Similarity 7; Conserv
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Pred.
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COPPER (POTENTIAL).
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26;
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SMART; SM00230; CysPc; 1.
SMART; SM00054; EFh; 2.
PROSITE; PS00018; EF_HAND;
PROSITE; PS000139; THIOL_PRC
PROSITE; PS00640; THIOL_PRC
PROSITE; PS00640; THIOL_PRC
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                                                                                                                                                                                                                                                                                                                                                                                                                      between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and foentities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 muscle expresses four distinct calpains.";
Biochim. Biophys. Acta 1261:381-33(1995).

-i-FUNCTION: Calcium-regulated non-lysosomal thiol-protease which catalyze limited proteolysis of substrates involved in cytoskeletal remodelling and signal tranduction (By similarity).

-i-CATALYTIC ACTIVITY: Preferential cleavage: Tyr-|-Xaa, Met-|-Xaa or Arg-|-Xaa with Leu or Val as the P2 residue.

-i-COPACTOR: Binds 3 calcium ions.

-i-ENZYME REGULATION: Activated by 200-1000 micromolar concentrations of calcium and inhibited by calpastatin.

-i-SUBUNIT: Heterodimer of a large (catalytic) and a small
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Calpain 2, large [catalytic] subunit precurso
(Calcium-activated neutral proteinase) (CANP)
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01-NOV-1997 (Rel.
15-JUN-2002 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAN2_CHICK
Q92178;
                                                                                                        PROPEP
CHAIN
                                                                                                                                                                                                                                         pfam; pF00036; efhand; 3.
pfam; pF00648; Peptidase_C2; 1.
pfam; pF01067; Calpain_III; 1.
pRINTS; PR00704; CALPAIN.
proDom; PD000012; EF-hand; 1.
                                                                                                                                                                                                                                                                                                                                                                               EMBL; D38026; HSSP; Q07009;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Identification of a third ubiquitous calpain species muscle expresses four distinct calpains.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Suzuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sorimachi H.,
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                                                                                                                                                                                                                                                                                                                                  InterPro;
                                                                                                                                                                                                                                                                                                                                                   InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (regulatory) subunit.
SUBCELLULAR LOCATION: Cytoplasmic; Translocates to the membrane upon Ca++ binding.
SIMILARITY: CONTAINS 5 EF-HAND CALCIUM-BINDING DOMAINS SIMILARITY: BELONGS TO PETTIDASE FAMILY C2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gallus (Chicken).
                                                                                                                                                                                                                                                                                                                    IPR001300; Protease_C2.
IPR000169; SHprot_acsite.
                                                                                                                                                                                                                                                                                                                                                   IPR002048;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tsukahara T., Okada-Ban M.,
                                                                                                                                                                                                                                                                                                                                                                               1DF0.
                                                                                                                                                                                                                                                                                                                                                                                              BAA07228.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                     protease;
                                                                                                                                                              EF_HAND; 2,
THIOL_PROTEASE_CYS;
THIOL_PROTEASE_HIS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           35, Created)
                                                                                                                                                   THIOL_PROTEASE_ASN;
    19
700
210
355
514
529
700
552
596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                   Protease_C2
                                                                                                                                                                                                                                                                                                                                                   EF-hand.
                                                                         COTEASE_ASN; FALSE_NEG.
Calcium-binding; Multigene family
ANCHORS TO THE SMALL SUBUNIT (PO
CALPAIN 2, LARGE [CATALYTIC] SUI
THIOL PROTEASE DOMAIN I.
THIOL PROTEASE DOMAIN II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                c] subunit precursor proteinase) (CANP) (
                                              DOMAIN 1
                                  DOMAIN IV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          700
                                                                                                                                                                     FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sugita
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (M-type) (M-calpain)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (EC 3.4.22.17)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     H., Ishiura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          chicken
                                                                                                                         (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     a collaboration - MBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                           for
                                                                                                                                                                                                                                                                                                                                                                                                                                             .ch/announce,
                                                                                                                                                                                                                                                                                                                                                                                                                                                           In no way
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ween the Swiss Institute of Bioinformatics European Bioinformatics Institute. There a

There are no restrictions ng as its content is in

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EMBL

a collaboration

Usage

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commercial

<u></u> 9 SWISS-PROT entry is copyright. It is produced through

the

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RESULT 13
SUF2_HUMAN STANDARD; PRT; 748 AA.
ID SUF2_HUMAN STANDARD; PRT; 748 AA.
AC Q9HAU4; Q9H260;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Smad ubiquitination regulatory factor 2 (EC 6.3.2.-
DE protein ligase SMURF2) (Smad-specific E3 ubiquitin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            õ
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Best Local S
Matches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CA_BIND
DOMAIN
DOMAIN
ACT_SITE
ACT_SITE
ACT_SITE
                                                                                                                                                                                                      SEQUENCE FROM N.A., AND MUTAGENESIS OF CYS-716.
MEDLINE-21107656; PubMed-11158580;
Zhang Y., Chang C., Gehiling D.J., Hemmati-Brivaniou A.,
"Regulation of Smad degradation and activity by Smurf2,
"Regulation of Smad degradation and activity by Smurf2,
"Proc. Natl. Acad. Sci. U.S.A. 98:974-979(2001).
-1- FUNCTION: Interacts with SMAD1, SMAD2 and SMAD7 in
                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A., AND MUTAGENESIS OF PROMEDITINE=20538422; PubMed=11016919; Lin X., Liang M., Feng X.-H.; "Smurf2 Is a ubiquitin E3 ligase mediating degradation of Smad2 in transforming growth 13 Biol. Chem. 275:36818-36822(2000).
                                                                                                                                                                                                                                                                                                                                                                                         Thomsen G.H., Wrana J.L.;
"Smad7 binds to Smurf2 to form an E3
"GF-beta receptor for degradation.";
Mol. Cell 6:1365-1373(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
Homo sapiens (Human).

"horia; Metazoa; Chordata; (horia; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., GLY-297--LEU-330.
                                                                                                                                                                                                                                                                                                                                                                                                                                            (avsak P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                           PubMed=11163210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hSMURF2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ₩.
                    TISSUE SPECIFICITY: Widely expressed.
DOMAIN: The second and third WW domains
interaction with R-SMAD (SMADI, SMAD2 ar
SIMILARITY: CONTAINS 1 C2 DOMAIN.
SIMILARITY: CONTAINS 1 WW DOMAINS.
SIMILARITY: CONTAINS 1 HECT-TYPE E3 UBIC
                                                                                                                               trigger their ubiquitination and proteasome-dependent degradat. Enhances the inhibitory activity of SMAD7 and reduces the transcriptional activity of SMAD2. Coexpression of SMURF2 with SMAD1 results in considerable decrease in steady-state level of SMAD1 protein and a smaller decrease of SMAD2 level.
SUBUNIT: Interacts with SMAD1, SMAD2, SMAD3, SMAD6 and SMAD7 by
                                                                                 SMAD7.
TISSUE SPECIFICITY:
                                                                                                       not SMAD4.
SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PEWPSYLGYEKLGP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity 57.1
8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                            Rasmussen
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650
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57.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Causing
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ANCESTRAL CALCIUM S
ANCESTRAL CALCIUM S
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
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Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C3AEDB39CCB56D3B
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                                                                                                        Cytoplasmic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QF
                                                                                                                                                                                                                                                                                                                                                                                                                                            .G.,
                    E3 UBIQUITIN-PROTEIN LIGASE
                                                                                                                                                                                                                                                                                                                   growth
                                                                                                                                                                                                                                                                                                                                                                                                                    ubiquitin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB
30;
                                                                                                                                                                                                                                                                                                                                                                    PRO-251--VAL-284 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRO-251--VAL-284 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                            Bonni
                                                       and SMAD3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hominidae;
                                                                                                                                                                                                                                                                                                               proteasome-dependent
h factor-beta signaling.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4.
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                                                                                                                                                                                                                                                                                                                                                                                                                    ligase that targets
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 700
                                                                                                                                                                                                                                            Smurf2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CRC64;
                                                                                                        the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (POTENTIAL).
                                                                                                       presence
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                                                                                                                                                                                                       order
                                                                                                                                                                                                                                           Derynck
an E3
                                                                                                                                                                                            degradation
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                                                                                                                                                                                                                                                                                                                                                                    CYS-716
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RESULT 14
CB2_MALDO
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                                                                                                                                                                           CB2_MALDO STANDARD; PRT; 268 AA. P15773;
01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
16-JUN-2002 (Rel. 41, Last annotation update)
17-JUN-2002 (Rel. 41, Last annotation update)
18-JUN-2002 (Rel. 41, Last annotation update)
19-JUN-2002 (Rel. 41, Last annotation ABB10, chlorop
19-JUN-2002 (Rel. 41, Last annotation ABB10, chlorop
19-JUN-2002 (Rel. 41, Last sequence update)
19-JUN-200
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Best Local :
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Pfam; PF00632: HECT; 1
SMART; SM00239; C2; 1
SMART; SM00219; HECTc; 1.
SMART; SM00119; HECTc; 1.
SMART; SM00416; WW; 3.
PROSITE; PS00499; C2_DOMAIN_1; 1.
PROSITE; PS50004; C2_DOMAIN_2; 1.
PROSITE; PS50027; HECT; 1.
PROSITE; PS50020; WW_DOMAIN_1; 1.
PROSITE; PS50020; WW_DOMAIN_2; 3.
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SEQUENCE
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EMBL; AF301463; AAG25641.1; -.
EMBL; AY014180; AAG50421.1; -.
HSSP; Q13526; 1PIN.
STRAIN-cv. Golden MEDLINE-90175017;
                                                                                                                                     Spermatophyta; Magnoliophyta; eurosids I; Rosales; Rosaceae;
                                                    SEQUENCE FROM N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MUTAGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                           NCBI_TaxID=3750;
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PF00397; WW; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IPR001202; WW_Rsp5_WWP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     748
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251
297
414
251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pathway;
Delicious; TISSUE=Leaf;
PubMed=2408025;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    716
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C2 [
                                                                                                                                  Streptophyta; Embryop
yta; eudicotyledons; co
ceae; Maloideae; Malus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MW;
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C->G: LOSS OF ACTO UBIQUITINATE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 45;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MISSING: ABOLISHES
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chloroplast
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                                                                                                                                                                                            Embryophyta; Tracheophyta;
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RESULT 15
LEU2_PYRAE
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"Nucleotide sequence of an apple nuclear gene encoding a light-
ray harvesting chlorophyll a/b binding polypeptide of photosystem II.";

RI Nucleic Acids Res. 18:679-679(1990).

C. HONGTION: THE LIGHT-HARVESTING COMPLEX (LHC) FUNCTIONS AS A LIGHT
C. FUNCTION: THE DIGHT-HARVESTING COMPLEX (LHC) FUNCTIONS AS A LIGHT
C. HONGTION: TI CAPTURES & DELIVERS EXCITATION ENERGY TO PHOTOSYSTEMS
C. WITH WHICH IT IS CLOSELY ASSOCIATED. THE N-TERMINUS OF THE PROTEIN
C. EXTENDS INTO THE STROMA WHERE IT IS INVOLVED WITH ADHESION OF
C. GRANAL MEMBRANES AND PHOTOSREGULATED BY REVERSIBLE PHOSPHORYLATION
C. OF ITS THREONINE RESIDUES; BOTH ARE BELIEVED TO MEDIATE THE
DISTRIBUTION OF EXCITATION ENERGY BETWEEN PHOTOSYSTEMS I AND II.
C. ISUBURIT: THE LHC COMPLEX CONSISTS OF CHLOROPHYLLS (A & B) AND
C. ISUBCULTAR LOCATION: Chloroplast thylakold membrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This
                                                                                                                                                                                                                                                                    Q8ZW41:
15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
3-isopropylmalate dehydratase large subunit (EC 4.2.1.33)
(Isopropylmalate isomerase) (Alpha-IPM isomerase) (IPMI).
LEUC OR PAE1984.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X17697; CAA35690.1; -.
PIR; S08229; S08229.
InterPro; IPR001344; Chloro_ABbind.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chlorophyll; Photosynthesis; Photosystem I; Photosystem II; Thylakoid; Membrane; Chloroplast; Transit peptide; Multigene family;
                                           aerophilum.";
Proc. Natl. Acad. Sci. U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00504;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ProDom;
                                                                                                     Miller J.H.
                                                                                                                 Fitz-Gibbon S.T., Ladner
                                                                                                                                  PubMed=11792869;
                                                                                                                                                    STRAIN=IM2 / ATCC 51768 / DSM 7523;
                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                  Thermoproteaceae; Pyrobaculum.
NCBI_TaxID=13773;
                                                                                                                                                                                                                                     Archaea; Crenarchaeota; Thermoprotei; Thermoproteales;
                                                                                                                                                                                                                                                    Pyrobaculum aerophilum.
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                                                                                  "Genome sequence of the hyperthermophilic crenarchaeon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
les 9; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation European Bioinformatics Institute. There are no restrictions on its
FUNCTION: Catalyzes the isomerization between 2-isopropylm and 3-isopropylmalate, via the formation of 2-isopropylmalate CATALYTIC ACTIVITY: 3-isopropylmalate = 2-isopropylmaleate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EWPSYLTGEFPGDY
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                                                                                                                 Kim U.-J.,
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                                                     99:984-989(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1CAA091F7AEC6303 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                       415
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17;
                                                                                                                     Stetter K.O.,
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               2-isopropylmaleate
                                    2-isopropylmalate
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Leucine biosynthesis; Lyase;
METAL 295 295
METAL 353 353
METAL 356 356
SEQUENCE 415 AA; 44747 MW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00450; ACONITASE_1; 1.
PROSITE; PS01244; ACONITASE_2; FP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00330; aconitase; ProDom; PD000511; Aconitas
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CATALYTIC ACTIVITY: 2-isopropylmaleate + H(2)O = isopropylmalate.

isopropylmalate.

PATHWAY: Leucine biosynthesis; second step.

PATHWAY: Heterodimer of leuC and leuD (By simila: SIMILARITY: BELONGS TO THE ACONITASE/IPM ISOMERA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SWISS-PROT entry is copyright. It is produced through sen the Swiss Institute of Bioinformatics and the EN
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7; Conser
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                                                                                                                                                                                                                                                                                            Conservative
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Heterodimer of leuC and leuD (By similarity).
TY: BELONGS TO THE ACONITASE/IPM ISOMERASE FAMILY. LEUC
                                                                                                                                                                                                                                                                                                                                                                                                                                 ACONITASE_2; FALSE_NEG.

ACONITASE_2; FALSE_NEG.

1515; Lyase; Iron-sulfur; 4Fe-4S; Complete proteome.

1525
1 IRON-SULFUR (4FE-4S) (BY SIMILARITY).

1535
1 IRON-SULFUR (4FE-4S) (BY SIMILARITY).

154747 MW; 2B28CA0921842473 CRC64;
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53.88;
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Pred. No.
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 283224 seqs, 96134422 residues
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(without alignments)
96.134 Million cell updates/sec
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45	44	43	42	41	40	39	38	37	36	35	34	3 3	32	31	30
42.5	42.5	43	43	43	43	43	43	43	43	43	43	43	43.5	44	44
42.9	42.9	43.4	43.4	43.4	43.4	43.4	43.4	43.4	43.4	43.4	43.4	43.4	43.9	44.4	44.4
735	401	2970	1296	1094	730	544	503	421	415	378	267	120	359	761	554
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ALIGNMENTS

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RESULT 2
$42394
G-box-binding protein - tomato
C;Species: Lycopersicon esculentum (tomato)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Ju
C;Accession: $42394
R;Meier, I.; Gruissem, W.
Nucleic Acids Res. 22, 470-478, 1994
A;Title: Novel conserved sequence motifs in plant G-box binding prot A;Reference number: $42392; MUID:94173701; PMID:8127687
A;Accession: $42394
A;Status: preliminary
A;Molecule type: mRNA
A:Residues: 1-406 <MEI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R:Moorhead, G.; MacKintosh, C.; Morrice, N.; Cohen, P.;

FEBS Lett. 362, 101-105, 1995

A;Title: Purification of the hepatic glycogen-associated form of protein phosp
A;Reference number: $68721; MUID:95237359; PMID:7720853

A;Accession: $68723

A;Molecule type: protein
A;Residues: 61-76;150-157 <MOO>
A;Experimental source: liver
C;Keywords: glycogen metabolism; phosphoric monoester hydrolase
F;1-284/Product: phosphoprotein phosphatase 1 glycogen-binding chain #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        phosphoprotein phosphatase (EC 3.1.3.16) 1 glycogen-binding chain - rat N.Alternate names: 33K protein glycogen-binding chain (G(L)) C;Species: Rattus norvegicus (Norvay rat) C;Date: 15-Fab-1997 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999 C;Accession: S68216; S74276; S68723 R;Doherty, M.J.; Moorhead, G.; Morrice, N.; Cohen, P.; Cohen, P.T.W. FEBS Lett. 375, 294-298, 1995 A;Fitle: Amino acid sequence and expression of the hepatic glycogen-binding (G(L))-su A;Reference number: S68216; MUID:96085228; PMID:7498521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: protein
A;Residues: 21-24;43-56;61-98;150-157;161-169;181-199;201-220;238-253;280-284 <DOE>
R;Moorhead, G.; MacKintosh, C.; Morrice, N.; Cohen, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Accession: S68216
A; Molecule type: mRNA
A; Residues: 1-284 <DOH>
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A; Accession: $74276
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Matches 16
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A;Cross-references: GB:M28704; NID:g170748; PIDN:AAA34293.1; PID:g170749 C;Superfamily: fava bean G-box-binding protein; fos/jun DNA-binding domai C;Keywords: DNA binding; nucleus; transcription regulation F;247-287/Domain: fos/jun DNA-binding domain box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box-in-box
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C;Date: 03-Apr-1992 #sequence_revision 03-Apr-1992 #text_change 09-Jun-2000
C;Accession: A41349
R;Tabata, T; Takase, H; Takayama, S; Mikami, K; Nakatsuka, A; Kawata, Science 245, 965-967, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C:Superfamily: calpain large chain; calmodulin repeat homology; calpain catalytic domain c;Keywords: calcium binding; cysteine proteinase; duplication; EF hand; heterodimer; hyd F:75-327/Domain: calpain catalytic domain homology <CALP>
F:529-560/Domain: calmodulin repeat homology <EF1>
F:572-604/Domain: calmodulin repeat homology <EF2>
F:605-634/Domain: calmodulin repeat homology <EF2>
F:607-669/Domain: calmodulin repeat homology <EF3>
F:637-669/Domain: calmodulin repeat homology <EF4>
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A; Residues: 380-439 <SAM>
A; Cross-references: EMBL: X51772
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A; Title: Molecular cloning and bacterial expression of A; Reference number: S38361; MUID:94032492; PMID:8218419
A; Accession: S38361
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                                                                                                                                                                                                                A; Molecule type: mRNA
A; Residues: 1-349 < TAB>
                                                                                                                                                                                                                                                                                                                 A; Title: A protein that binds to a cis-acting element of wheat histone genes A; Reference number: A41349; MUID:89368924; PMID:2772648
A; Accession: A41349
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A; Accession: S08650
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 1-700 < DEL>
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C;Superfamily: fava bean G-box-binding protein; fos/jun DNA-binding domain
                                                                                                                                                                                                                                                                                    A; Status: preliminary
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                                                                       DNA-binding domain
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Pred. No.
Score 51;
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Length 349
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A;Reference number: S15346;
A;Recession: S15346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 1-18 <MIW>
R; Tabata, T.; Nakayama, T.;
EMBO J. 10, 1459-1467, 1991
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A; Residues: 1-349 < TAB>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N; Alternate
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Biol. Chem. Hoppe-Seyler 371(Suppl.), 171-176, 1990
A;Title: A novel member of the calcium-dependent cysteine p
A;Reference number: S10589; MUID:90380278; PMID:2400579
A;Accession: S10590
A;Molecule + manual control of the calcium 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C:Species: Homo sapiens (man)
C:Date: 21-Nov-1993 #sequence_revision 09-Aug-1997
C:Accession: S10590; A31218; A33529
R:Sorinachi, H.; Ohmi, S.; Emori, Y.; Kawasaki, H.;
A; Molecule type: mRNA
A; Residues: 1-700 <SON>
A; Residues: 1-700 <SON>
R; Imajoh, S.; Aoki, K.; Ohno, S.; Emori, Y.; Kawasaki, H.; Su
Biochemistry 27, 8122-8128, 1988
A; Title: Molecular cloning of the cDNA for the large subunit
A; Reference number: A31218; MUID:89166474; PMID:2852952
A; Accession: A31218
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A;Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 names: calpain chain L-2; calpain II catalytic chain; high-calcium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3.4.22.17) large chain 2 - human
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leucine zipper protein HBP-la(17)
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                                                                                                                                                                                                           Sugihara, H.; Suzuki,
                                                                                                          of the high-Ca(2+)-requi
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A; Description: catalyzes the hydolysis of peptides
A; Note: Cleaves preferentially after tyrosine, methionine, or arginine residues and befc
C; Superfamily: calpain large chain: calmodulin repeat homology; calpain catalytic domain
C; Keywords: acetylated amino end; calcium binding; cysteine proteinase; EF hand; heterod
F; 2-700/Product: calpain large chain 2 #status predicted AMATY
F: 75-327/Domain: calpain catalytic domain homology <CALPY
F; 529-560/Domain: calmodulin repeat homology <EF1>
F; 529-560/Domain: calmodulin repeat homology <EF2>
F; 605-634/Domain: calmodulin repeat homology <EF2>
F; 637-669/Domain: calmodulin repeat homology <EF4>
F; 637-669/Domain: calmodulin 
                                     A:Note: cleaves preferentially after tyrosine, methionine, or arginine residues and before the protest of the p
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A:Residues: 1-210,'I', 212-394,'D',396-445,'I',447-700 <IMA>
A:Residues: 1-210,'I',212-394,'D',396-445,'I',447-700 <IMA>
A:Residues: GB:M23254; NID:g511636; PIDN:AAA35645.1; PID:g511637
A:Note: parts of this sequence were determined by protein sequencing; the
R:Hata, A.; Ohno, S.; Akita, Y.; Suzuki, K.
J. Biol. Chem. 264, 6404-6411, 1989
A:Title: Tandemly reiterated negative enhancer-like elements regulate transference number: A33529; MUID:89197947; PMID:2539381
A:Accession: A33529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A:Introns: 82/3; 106/1; 145/3; 190/2; 246/3; 274/3; 303/2; C:Complex: heterodimer of L (large) and S (small) chains C:Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       calpain (EC 3.4.22.17) large chain 4 - chicken
N;Alternate names: calpain catalytic chain; intermediate calcium activated |
C;Species: Gallus gallus (chicken)
C;Date: 17-May-1985 #sequence_revision 09-Aug-1997 #text_change 24-Nov-1999
C;Accession: A00979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GDB:119750; OMIM:114230
A;Map position: lpter-lqter
C;Complex: heterodimer of L (large) and S (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Contents: annotation; C; Comment: This calpain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A:Cross-references: EMBL:X01415; NID:g63332; PIDN:CAA25658.1; R;Emor1, Y.; Ohno, S.; Tobita, M.; Suzuki, K. FEBS Lett. 194, 249-252, 1986
A:Reference number: A91354; MUID:86082358; PMID:3000828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Title: Evolutionary origin of a calcium-dependent protease by A;Reference number: A93348; MUID:85061606; PMID:6095110 A;Accession: A00979
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A; Residues: 1-67,'G',69-72,'IE',75-78,'R' <HAT>
A; Cross-references: DDBJ:J04700; NID:g179910; PIDN:AAA52760.1;
                                                                                                                                                                                                                                                                                                                                                                                                             A; Description: catalyzes the hydolysis of peptides
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     ;609-638/Domain: calmodulin;641-673/Domain: calmodulin
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hypothetical protein MOAC9.6b - Caenorhabditis elegans C:Species: Caenorhabditis elegans C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #te C:Accession: T23713 R:Burton, J. submitted to the EMBL Data Library, December 1996 A:Reference number: Z19787
                                                                                                                                                                                                                                                                                                                                                                        RESULT
T23713
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                                                                                                                                                                                         A;Status: preliminary; translated
A;Molecule type: DNA
A;Residues: 1-1160 <WILL>
A;Cross-references: EMBL:Z83731; I
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F;2/Modified site: blocked amino end (Met) (in mature form)
F;108,265,289/Active site: Cys, His, Asn #status predicted
                                                                                                               A; Map position: 1
A; Introns: 71/3; 91/3;
                                                                                                                                                             A; Experimental source: C; Genetics:
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                          2 EWPSYLGYEKLGPY
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KWVSFIAYQQLGPF
                                                                                                                                                                                                                                                                                                                                                                                                                                    KWVSFIAYQQLGPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71/3; 91/3;
                                                       Similarity 42.66; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity 42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                           EMBL: Z83731; PIDN: CAB06024.1; GSPDB: GN00019; CESP: M04C9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL: Z83731; PIDN: CAB54273.1; GSPDB: GN00019; CESP: M04C9.6c
                                                                                                                  114/3;
                                                                                                                                                                           clone M04C9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     114/3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                clone M04C9
158
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53.3%;
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                                                                                                                262/2; 322/2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     262/2; 322/2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 49;
Pred. No.
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Pred. No.
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23;
                                                                                                               374/1;
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                                                                                                                461/2;
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                                                                                   Length 1160
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R.She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Away Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J. submitted to GenBank, April 2001
A;Description: Sulfolobus solfataricus complete genome.
A;Reference number: A99139
A;Accession: H90159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-127 <TRNA
C;Superfamily: immunoglobulin V region; immunoglobulin
C;Keywords: heterotetramer; immunoglobulin
F;15-97/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ig heavy chain V region (PAC1) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 20-Jul-1989 #sequence_revision 20-Jul-1989 #text_change 23-May-1997
C:Accession: B31807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein M04C9.6a - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #te: C;Accession: T23714
A;Cross-references:
C;Genetics:
A;Gene: lig
                                                                                                                                                                                                                                                                hypothetical protein lig [imported] - Sulfolobus solfataricus c;Species: Sulfolobus solfataricus C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 15-Jun-2001 C;Accession: H90159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Title: A monoclonal antibody against the platelet fibrinogen receptor contains a sequence number: A31807; MUID:89079661; PMID:2909518
A;Accession: B31807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R; Taub, R.; Gould, R.J.; Garsky, J. Biol. Chem. 264, 259-265, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Reference number: A; Accession: T23714
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A; Introns: 71/3; 91/3; 114/3; 262/2;
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A;Cross-references: EMBL:Z83731; PIDN:CAB06025.1; GSPDB:GN00019; CESP:M04C9.
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                                                         A; Molecule type: DNA
A; Residues: 1-601 < KUR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                   A;Status: preliminary
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Best Local
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les 8; Conserv
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                                        GB:AE006641; NID:g13813323; PIDN:AAK40535.1; GSPDB:GN00155
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                                                                                                                                                                                                                                                                                                                                                                                                                                  112
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Pred. No.
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Pred. No.
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26;
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172 EWPPLLGYNKL 182

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probable morphine 6-dehydrogenase - Pyrococcus horikoshii
C;Speciles: Pyrococcus horikoshii
C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change
C;Accession: D71221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change C;Accession: AG0701 R; James, K.D.; Thomson, N.R.; Pickard, R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, Thomson, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA Res. 5, 55-76, 1998
A; Title: Complete sequence and gene organization of the A; Reference number: A71000; MUID:98344137; PMID:9679194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Kawarabayasi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
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                                                                                                                                                                                                                                               A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-245 <PAR>
                                                                                                                                                                                                                                                                                                                                                       A; Ruthors: Parry, C.; Quail, M.; Rutherford, K.; A; Authors: Parry, C.; Quail, M.; Rutherford, K.; A; Title: Complete genome sequence of a multiple ca; Reference number: AB0502; PMID:11677608
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C; Superfamily: aldehyde reductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:AP000001; NID:g3236128; PIDN:BAA29099.1; A;Experimental source: strain OT3
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A;Molecule type: DNA
A;Residues: 1-273 <KAW>
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Orf 245 protein [imported] - Salmonella enterica subsp. enterica serovar Typhi
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                                                                                                                                                                   A;Gene:
                                                                                                                                                                                                                     A;Cross-references: GB:AL513382; PIDN:CAD01984.1; PID:g16502824; GSPDB:GN00176
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Best Local Similarity
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                                                                                                                                                                   STY1741
  EWPSYLGYEKL 12
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8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.;
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protein kinase (EC 2.7.1.37) cdc2-related CRK1 - Leishmania mexicana
C:Species: Leishmania mexicana
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A48041; S31366
R:Mottram, J.C.; Kinnaird, J.H.; Shials, B.R.; Tait, A.; Barry, J.D.
J. Biol. Chem. 268, 21044-21052, 1993
A:Title: A novel CDC2-related protein kinase from Leishmania mexicana, LmmCRK1, is post-A:Reference number: A48041; MUID:94012652; PMID:8407941
A:Accession: A48041
A;Status: nucleic acid sequence not shown
A:Residues: 1-301 cMOT>
A;Cross-references: EMBL:X60385; NID:99539; PIDN:CAA42936.1; PID:99540
C:Superfamily: kinase-related transforming protein; protein kinase homology
C:Keywords: ATP: phosphotransferase
F:3-257/Domain: protein kinase homology <KIN>
F:11-19/Region: protein kinase ATP-binding motif
F:34,52,127,129/Active site: Lys, Glu, Asp, Lys #status predicted
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Search completed: January 13, 2003, 14:34:48 Job time: 18 secs
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251 PEWSNVLGSVPGYEKLG 267
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                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                of hits satisfying chosen parameters:
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1: /cgn2_6/ptodata/1

2: /cgn2_6/ptodata/1

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US-08-868-435-31
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	DB .3e s				rsion #	Beecham Corporation Road	tase 1	STN	-604A-26 -496A-26 -136-26 -839-8 -839-4 -839-4 -839-2 -839-2 -839-2 -136-28 -718-28 -718-3 -718-3 -718-3
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	Gaps								26, Appl 26, Appl 26, Appl 6, Appl 12, Appl 12, Appl 22, Appl 23, Appl 28, Appl 28, Appl 28, Appl 28, Appl 31, Appl 31, Appl 31, Appl 33, Appl 33, Appl 33, Appl 33, Appl 33, Appl
	0;								

RESULT 2 US-09-480-203-3

Patent No.

3, Application US/09480203 o. 6297359

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APPLICANT: PATTICIA T.W. Cohen
APPLICANT: Phillip Cohen
APPLICANT: Peter R. Young
TITLE OF INVENTION: A PROTEIN PHOSPHATASE 1 BINDING PROTEIN
TITLE OF INVENTION: R5
FILE REFERENCE: ATG-5003-2
CURRENT APPLICATION NUMBER: US/09/480,203
CURRENT FILING DATE: 2000-01-10
EARLIER APPLICATION NUMBER: 09/300,327
EARLIER APPLICATION NUMBER: 09/300,327
EARLIER FILING DATE: 1999-04-27
EARLIER FILING DATE: 1996-12-05
NUMBER OF SEO ID NOS: 6
SOFTWARR: FastSEQ for Windows Version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 3
LENGTH: 284
TYPE: PRT
ORGANISM: HOMO SAPIENS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
TELECOMMUNICATION INFORMATION: TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Lin, Lih-Ling
APPLICANT: Graham, James
TITLE OF INVENTION: INTERLEUKIN-1 RECEPTOR
TITLE OF INVENTION: INTRACELLULAR LIGAND PROTEINS AND INHIBITORS OF LIGAND
TITLE OF INVENTION: BINDING
                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/487,942
APPLICATION NUMBER: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       269 PEWPSYLGYEKLGPYY 284
                                                                                                                                                                                                             APPLICATION NUMBER: US/08/726,525 FILING DATE: 07-OCT-1996 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 87 Cambridge
                                                                     REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 02140
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                                                                                                                                                                                                                                                                                                                                                                                                                          USA
                                                                                                                                                                                                                                                                                                                   TE: Floppy disk

IBM PC compatible

SYSTEM: PC-DOS/MS-DOS
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Pred. No. 1.3e-07;
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RESULT

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                                                    Best Loc
Matches
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Best Local (
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                                                                              Query Match
                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: BIOWN, SCOUT A.
REGISTRATION NUMBER: 32,724
REFERENCE/DOCKET NUMBER: G152
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                        TELEFAX: (617) 876-585
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 700 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 700 amino acid
                                                                                                                                      MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Lin, Lih-Ling APPLICANT: Graham, James
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
52
                                                                                                                                                STRANDEDNESS:
TOPOLOGY: lin
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                                                    Local Similarity 60.0 tosal Similarity
                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/487,942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE:
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                        1 PEWPSYLGYEKLGPY 15
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                                                                                                                                                                            amino acid
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                                                                                                                                                                                        700 amino acids
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(617) TD NO: 7:
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                                                   Score 51; DB
Pred. No. 6.2;
3; Mismatches
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                                                                   DB 2;
6.2;
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US-08-726-036A-7

Application US/08726036A

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US-09-422-869-23
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TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 700 anino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patent No. 5981482
                                                                                                                                                                                                                                                                                                                                       Sequence 23, Appl. Patent No. 6235481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 60.0
Matches 9; Conservative
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                                                                                                                                                                                              APPLICANT: ODA, NAOHISA
APPLICANT: COX, NANCY J.
APPLICANT: SREENAN, SEAMUS
APPLICANT: ZHOU, YUN-PING
APPLICANT: OTANI, KENICHI
APPLICANT: HANIS, CRAIG L.
APPLICANT: BELL, GRAEME I.
APPLICANT: BELL, GRAEME I.
TITLE OF INVENTION: METHODS OF TREATMENT OF TYPE 2 DIABETES
FILE REFERENCE: ARCD: 307
CURRENT FILING DATE: 1999-10-21
CURRENT FILING DATE: 1999-10-21
EARLIER APPLICATION NUMBER: 60/134,175
EARLIER FILING DATE: 1999-05-13
NUMBER OF SEQ ID NOS: 30
                                                                                                                                                                                                                                                                               APPLICANT: POLONSKY, KENNETH APPLICANT: HORIKAWA, YUKIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/726,036A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Lin, Lih-Ling
APPLICANT: Graham, James
TITLE OF INVENTION: NOVEL INTERLEUKIN-1 RECEPTOR
TITLE OF INVENTION: INTRACELLULAR LIGAND PROTEINS AND INHIBITORS OF LIGAND
TITLE OF INVENTION: BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52
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CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: sir
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STREET: 87 CambridgePark Drive
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; MOLECULE TYPE:
; HYPOTHETICAL:
US-09-083-516-7
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Best Local Similarity
Thehes 9; Conserve
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                                                                                                                                                 Query Match
Best Local (
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                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 7, Application US/09083516 Patent No. 6300086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (617) 876-58 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: INVITITE OF INVENTION: INVITION: INVITION: BIT INVENTION: BIT INVENTION: BIT INVITION: BIT INV
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ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPAS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
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52
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                                                        1 PEWPSYLGYEKLGPY 15
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   PAIPSALGFKELGPY
                                                                                                                 Similarity 60.0
9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                          amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                             700 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (617) 876-5851
TD NO: 7:
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Pred. No. 6
                                                                                                                    Mismatches
                                                                                                                                                 DB 4;
6.2;
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RESULT 8

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US-09-540-448-12
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APPLICANT: Unger, Evan C
APPLICANT: Wu, Yungiu
TITLE OF INVENTION: Optacoustic Contrast Agents and Methods For FILE REFERENCE: UNGR1224
CURRENT APPLICATION NUMBER: US/08/993,165A
CURRENT EILING DATE: 1997-12-18
NUMBER OF SEQ ID NOS: 40
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 12
LENGTH: 19
TYPE: PRT
                         GENERAL INFORMATION:
APPLICANT: Unger, Evan C
APPLICANT: Wu, Yunqiu
TITLE OF INVENTION: Optacoustic Contrast Agents And Methods For Their Use
FILE REFERENCE: UNGR1224
CURRENT APPLICATION NUMBER: US/08/993,165A
CURRENT FILING DATE: 1997-12-18
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LENGTH: 19
TYPE: PRT
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Best Local S
Matches 8
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Patent No. 6123923
                                                                                                                                                           Sequence 13, Application US/08993165A Patent No. 6123923
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PRIOR FILING DATE: 1997-09-08
NUMBER OF SEQ ID NOS: 37
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CURRENT FILING DATE: 2000-03-31
NUMBER OF SEQ ID NOS: 40 SOFTWARE: Patentin Ver. 2
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Local Similarity 61.5%;
nes 8; Conservation
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nes 8; Conservative
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                                                                                                                                                                                                                                                                                                               RESULT 12
5196510-15
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US-09-540-448-13
Sequence 13, Application US/09540448
Patent No. 6403056
                                                                                                                                                                                                                           ; APPLICANT: RODWELL, JOHN D.; MCKEARN, THOMAS J.; ALVAREZ, IVERNON, L.; RADCLIFFE, ROBERT D.
TITLE OF INVENTION: MOLECULAR RECOGNITION UNITS; NUMBER OF SEQUENCES: 43
CURRENT APPLICATION DATA:
                                                                                                                                          SEQ ID NO:15:
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                                                      Query Match
Best Local S
Matches 8
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SEQ ID NO 13
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Matches 8; Conser
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LENGTH: 21
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CURRENT FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: 08/925,353
PRIOR FILING DATE: 1997-09-08
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TITLE OF INVENTION:
FILE REFERENCE: UNG
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TYPE: PRT
ORGANISM: Artificial Sequence
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APPLICATION NUMBER: 2
                                                                                                                                                                                                 APPLICATION NUMBER: US, FILING DATE:07-MAY-1990
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tes 8; Conserv
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8; Conserv
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                                                      Conservative
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Pred. No. 0.44;
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Pred. No. 0.44;
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Pred. No. 0.
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                                                                    DB 6;
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APPLICANT: VOGEL, NUIL
APPLICANT: WYSS, MBrkus
FITLE OF INVENTION: MODIFIED PHYTASES
FILE RETERENCE: MODIFIED Phytases
CURRENT APPLICATION NUMBER: US/09/044,718
CURRENT FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: EP 97810175.6
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5196510-12
; Patent No.
                                                                                                     US-08-868-435-31
: Sequence 31, Application US/08868435
: Patent No. 6291221
: GENERAL INFORMATION:
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; TYPE: PRT
; ORGANLEM: Talaromyces thermophilus
US-09-044-718-9
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US-09-044-718-9
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APPLICATION NUMBER: 291,730
FILING DATE: 29-DEC-1988
SEQ ID NO:12:
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TITLE OF INVENTION: MOLECULAR RECOGNITION UNITS
NUMBER OF SEQUENCES: 43
CURRENT APPLICATION DATA:
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Best Local Similarity 61.5%;
Matches 8; Conservative
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Best Local Similarity
Matches 8; Conserv
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SEQ ID NO 9
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APPLICANT:
APPLICANT:
                         APPLICANT: Van Loon, Adolphus APPLICANT: Mitchell, David TITLE OF INVENTION: POLYPEPTII NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                               269 EWQAYDYYQSLGKYY 283
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                 ADDRESSEE:
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3: Hoffmann-La Roche Inc
340 Kingsland Street
                                                                                                                                                                                                                                                                             Conservative
                                              POLYPEPTIDES WITH PHYTASE ACTIVITY 35
                                                                                                                                                                                                                                                                                          48.5%;
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mismatches
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Pred. No. 0.57;
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Search completed: January 13, 2003, 14:35:08 Job time: 15 secs
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Best Local Similarity
""" B; Conserve
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy (
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COUNTRY: Uni
TD: 07110
                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: /note="potential N-glycosylation site" FEATURE: misc_feature LOCATION: 269 OTHER INFORMATION: /note="potential N-glycosylation site" FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Kass, Alan P
REGISTRATION NUMBER: 32142
REFERENCE/DOCKET NUMBER: Co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/868,435
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                         FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein FEATURE:
                                                               285
                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature LOCATION: 348
OTHER INFORMATION: /not
                                                                                                                                                                                                       NAME/KEY: misc_feature LOCATION: 372
OTHER INFORMATION: /not
                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature LOCATION: 335
OTHER INFORMATION: /no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 466 amino acids
TYPE: amino acid
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature
LOCATION: 204
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TELEFAX: (
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201) 235-2363
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Maximum DB seq length: 2000000000
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Perfect score:
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Published_Applications_AA:*

1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*

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7: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

9: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*

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13: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*

14: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
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Gapop 10.0 , Gapext 0.5
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

19	18	17	16	15	14	13	12	11	10	9	000	7	o	ı U	4	· w			Result No.
41	41	41	41.5	42	42	42	42	42	43	43	45	47	48	51	51	99	99	99	Score
41.4	41.4	41.4	41.9	42.4	42.4	42.4	42.4	42.4	43.4	43.4	45.5	47.5	48.5	51.5	51.5	100.0	100.0	100.0	Query Match
1247	1247	1246	152	1295	714	425	383	343	300	111	385	703	466	700	700	285	284	282	Query Match Length
10	10	10	10	10	10	10	10	10	10	10	10	10	12	10	10	10	10	10	DB
US-09-815-242-13841	US-09-815-242-10145	US-09-741-669-349	US-09-815-242-13962	US-09-726-949A-1	US-09-768-877-22	US-09-288-326-9	US-09-852-399-4	US-09-794-960-4	US-09-794-960-5	US-09-899-896-7	US-09-837-751-4	US-09-768-877-27	US-10-083-452-13	US-09-768-877-23	US-09-840-707A-9	US-09-737-149-12	US-09-737-149-42	US-09-737-149-43	ID
	10145		139	Sequence 1, Appli	Sequence 22, Appl	Sequence 9, Appli	Sequence 4, Appli	4	υ,	7,	Sequence 4, Appli	27,	Sequence 13, Appl	Sequence 23, Appl	Sequence 9, Appli	•	Sequence 42, Appl	Sequence 43, Appl	Description

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	
38	38	38	38	38	39	39	39	39	39	39	39	39	39	40	40	40	40	40	40.5	40.5	40.5	40.5	41	41	4
38.4	38.4	38.4			39.4	39.4	39.4		39.4	39.4	•	39.4	39.4	40.4	40.4	40.4	40.4	40.4	40.9	40.9	40.9	40.9	41.4	41.4	4 1 . 4
467	412	273	270	109	712	646	646	646	579	561	545	161	124	950	526	520	520	465	565	447	447	446	2972	1261	1 6 1 0
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US-10-083-452-9	US-10-090-624-1	US-09-925-297-695	US-09-923-779-152	US-09-729-674-118	US-09-864-761-34550	US-10-154-452-8	US-10-154-452-4	US-10-072-621-9	US-09-925-300-1415	US-09-821-687-4	US-09-978-242-1	US-09-821-687-2	US-09-864-761-33551	US-09-815-242-11271	US-09-925-300-1473	US-09-726-643-102	US-10-042-141-102	US-10-083-452-8	US-09-895-860-5	US-09-972-528-4	US-09-908-928-4	US-09-798-029-17	US-08-424-550B-387	US-09-815-242-11963	
9	1, A	Sequence 695, App	Sequence 152, App	Sequence 118, App	Sequence 34550, A	Sequence 8, Appli	Sequence 4, Appli		Sequence 1415, Ap	٠.	<u>ب</u>	Sequence 2, Appli	Sequence 33551, A	Sequence 11271, A	Sequence 1473, Ap	'n	102,	Sequence 8, Appli	Sequence 5, Appli	4	Sequence 4, Appli	Sequence 17, Appl	Sequence 387, App	Sequence 11963, A	de level annual

ALIGNMENTS

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; FEATURE: OTHER INFORM NAME/KEY: VA LOCATION: (1 OTHER INFORM OTHER INFORM OTHER INFORM OFFER INFORM	PRIOR FILIN NUMBER OF S SOFTWARE: P SEQ ID NO 43 SEQ ID NO 43 TYPE: PRT ORGANISM:	PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR	GENERAL INFORMATION: APPLICANT: Spaderna APPLICANT: Spinker APPLICANT: Stinker APPLICANT: Stinker APPLICANT: Muralid APPLICANT: Muralid APPLICANT: Muralid FILE REFERENCE: 159 CURRENT APPLICATION CURRENT APPLICATION PRIOR APPLICATION PRIOR APPLICATION N	RESULT 1 US-09-737-149-43 US-09-737-149-43 Sequence 43, Application US/09737149
FEATURE: OTHER IN NAME/KEY LOCATION OTHER IN OTHER IN 9-737-14	PRIOR FIL NUMBER OF SOFTWARE: SOFTWARE: EQ ID NO LENGTH: TYPE: PR ORGANISM		ENERAL IN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN TITLE OF FILE REFURENT CURRENT PRIOR AF	1 737 ienc
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FEATURE: OTHER INFORMATION: CONTER INFORMATION: CARIANT LOCATION: (1)(282) OTHER INFORMATION: WOTHER INFORMATION: WOTHER INFORMATION: SP737-149-43	G DATE: 200 EQ ID NOS: atentIn Ve 2 Artificial		ENERAL INFORMATION: APPLICANT: Spaderna, APPLICANT: Quinn, K APPLICANT: Shimkets APPLICANT: Muralidh APPLICANT: Mytek, TITLE OF INVENTION: FILE REFERENCE: 1596 CURRENT APPLICATION CURRENT FILING DATE: PRIOR APPLICATION NU PRIOR FILING DATE:	ica
25 6	SEQ ID NOS: 49 PatentIn Ver. 43 282 Ratificial Se	APPLICATION NUMBER: FILING DATE: 1999-12 APPLICATION NUMBER: FILING DATE: 1999-13 APPLICATION NUMBER: FILING DATE: 1999-13 FILING DATE: 2000-01 EAPPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER:	, St Kerr S, R hara Kim Pol Pol NUM NUM BE 2	tion
Consensus) Where X i subject s	FILING DATE: 2000-08-09 FILING DATE: 2000-08-09 RE: PATENTIN Ver. 2.0 NO 43 NO 43 PRT	UMBER: 60/ 1999-12-27 1UMBER: 60/ 1999-12-27 1UMBER: 60/ 1009-12-29 1UMBER: 60/ 2000-01-04/ UMBER: 60/	ENERAL INFORMATION: Steven K APPLICANT: Spaderna, Steven K APPLICANT: Shimkets, Richard APPLICANT: Shimkets, Richard APPLICANT: Muralidhara, Padi APPLICANT: Spytek, Kimberly, TITLE OF INVENTION: Polypepti FILE REFERENCE: 15966-620 CIP CURRENT APPLICATION NUMBER: 0/ CURRENT FILING DATE: 1999-12-14 PRIOR FILING DATE: 1999-12-14	US
m to	2000-08-09 1005: 49 1 Ver. 2.0	60/173, 2-27 60/173, 2-27 2-27 2-29 2-29 60/174, 1-04 1-04	ANT: Spaderna, Steven K ANT: Spaderna, Steven K ANT: Shinkets, Richard A. ANT: Shinkets, Richard A. ANT: Muralidhara, Padigaru ANT: Mythekets, Rimberly A. OF INVENTION: Polypeptides and DEFERENCE: 15966-520 CIP T APPLICATION NUMBER: US/09/73 T ETLING DATE: 2001-06-15 APPLICATION NUMBER: 60/170,564 FILING DATE: 1999-12-14	/097
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PRIOR FILING DATE: 1999-12-27
PRIOR APPLICATION NUMBER: 60/173,362
PRIOR FILING DATE: 1999-12-27
PRIOR APPLICATION NUMBER: 60/173,544
PRIOR APPLICATION NUMBER: 60/174,404
PRIOR APPLICATION NUMBER: 60/174,404
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SEQ ID NO 42
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                                                                                  APPLICANT: Muralidhara, Padigaru
APPLICANT: Spytek, Kimberly A.
TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding
FILE REFERENCE: 15966-620 CIP
CURRENT APPLICATION NUMBER: US/09/737,149
CURRENT FILING DATE: 2001-06-15
                PRIOR APPLICATION NUMBER: 60/170,564
PRIOR FILING DATE: 1999-12-14
PRIOR APPLICATION NUMBER: 60/173,165
PRIOR FILING DATE: 1999-12-27
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NUMBER OF SEQ ID NOS: 49
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CURRENT FILING DATE: 2001-06-15
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APPLICANT: Spytek, Kimberly A.
TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same
FILE REFERENCE: 15966-620 CIP
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Quinn, Kerry E.
Shimkets, Richard A.
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Shimkets, Richard A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 99; Ub ...
nred. No. 7.5e-08;
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Pred. No. 7.4e-08;
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                              Sequence 23, Application US/09768877 Patent No. US20020150896A1 GENERAL INFORMATION:
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RESULT 5
US-09-768-877-23
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                                                                                                                                                                                                                                                        US-09-840-707A-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 9
LENGTH: 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Fredeking, Terry M.
APPLICANT: Ignatyev, George M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 12
LENGTH: 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 9, Application US/09840707A Patent No. US20020077276A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 100. Matches 16; Conservative
                                                                                                                                                                                     Query Match
Best Local S
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                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Ignatyev, George M.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING HEMORRHAGIC VIRUS
TITLE OF INVENTION: IMPECTIONS AND OTHER DISORDERS
FILE REFERENCE: 24881-301C
CURRENT APPLICATION NUMBER: US/09/840,707A
CURRENT FILING DATE: 2001-04-23
PRIOR APPLICATION NUMBER: 09/562,979
PRIOR APPLICATION NUMBER: 09/562,979
PRIOR APPLICATION NUMBER: 60/198,210
PRIOR RELING DATE: 2000-04-27
PRIOR FILING DATE: 1999-04-27
                                                                                                                                                                                                                                                                     OTHER INFORMATION: IL-1 receptor intracellular ligand protein OTHER INFORMATION: comprising amino acid sequence PUBLICATION INFORMATION: PATENT DOCUMENT NUMBER: 5,817,476 PATENT FILING DATE: 1995-06-07 PUBLICATION DATE: 1998-10-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 60/223,929
PRIOR FILING DATE: 2000-08-09
NUMBER OF SEQ ID NOS: 49
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR FILING DATE: 1999-12-27
PRIOR APPLICATION NUMBER: 60/173,544
PRIOR FILING DATE: 1999-12-29
PRIOR APPLICATION NUMBER: 60/174,404
PRIOR FILING DATE: 2000-01-04
PRIOR APPLICATION NUMBER: 61/174,962
PRIOR FILING DATE: 2000-01-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 26
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TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
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                                                                                                                                                                    Local Similarity
nes 9; Conserv
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                                                                                                                        1 PEWPSYLGYEKLGPY 15
                                                                                  PAIPSALGFKELGPY 66
                                                                                                                                                                      Conservative
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Pred. No. 7.5e-08;
                                                                                                                                                                      Mismatches
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APPLICANT: POLONSKY, KENNETH S. APPLICANT: HORIKAWA, YUKIO

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                                                                                                                                                                                                                                  ; TYPE: PRT ; ORGANISM: Talaromyces thermophilus US-10-083-452-13
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: SEO ID NO 23
: LENGTH: 700
: TYPE: PRT
: ORGANISM: Human
US-09-768-877-23
RESULT 7
US-09-768-877-27
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APPLICANT: HANIS, CRAIG L.
APPLICANT: BELL, GRAEME I.
APPLICANT: BELL, GRAEME I.
TITLE OF INVENTION: METHODS OF TREATMENT OF TY
FILE REFERENCE: ARCD:307
CURRENT APPLICATION NUMBER: US/09/768,877
CURRENT FILING DATE: 2001-01-23
PRIOR APPLICATION NUMBER: 09/422,869
PRIOR FILING DATE: 1999-10-21
NUMBER OF SEQ ID NOS: 30
                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: PA 1998 00407
PRIOR FILING DATE: 1998-03-23
PRIOR APPLICATION NUMBER: PA 1998 00806
PRIOR ETLING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: PA 1998 01176
PRIOR APPLICATION NUMBER: PA 1998 01176
PRIOR FILING DATE: 1998-09-18
PRIOR APPLICATION NUMBER: PA 1999 00091
PRIOR FILING DATE: 1999-01-22
PRIOR APPLICATION NUMBER: 60/080,129
PRIOR FILING DATE: 1998-03-31
PRIOR FILING DATE: 1998-03-31
                                                                                                                                       Query Match
Best Local Similarity 53.3
                                                                                                                                                                                                                                                                                                                      SEQ ID NO 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence 13, Application US/10083452
Patent No. US20020127218A1
GENERAL INFORMATION:
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Matches 9; Conserv
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TITLE OF INVENTION: Phytase Variants
FILE REFERENCE: 5618.500-US
CURRENT APPLICATION NUMBER: US/10/083,452
CURRENT FILING DATE: 2002-02-26
                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 60/090,675
PRIOR FILING DATE: 1998-06-25
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSEQ for Windows Version 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT FILING DATE: 2002-02-26
PRIOR APPLICATION NUMBER: US/09/273,871
PRIOR FILING DATE: 1999-03-22
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                                                                      285 EWQAYDYYQSLGKYY 299
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COX, NANCY J.
SREENAN, SEAMUS
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53.3%;
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Pred. No. 2.7;
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                                                                                                                                                         Mismatches
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                                                                                                                                                                                           Length 466
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RESULT 9 US-09-899-896-7

Sequence 7, Application US/09899896
Patent NO. US20020072588A1
GENERAL INFORMATION:
APPLICANT: von Bdingen, Hans-Christ
APPLICANT: Genain, Claude P.

von Bdingen, Hans-Christian Genain, Claude P.

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Query Match
Best Local Similarity
7; Conserva
 В
                                                                                                                        ; LENGTH: 385
; TYPE: PRT
; ORGANISM: Gossypium sp.
US-09-837-751-4
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; ORGANISM: RAT
US-09-768-877-27
                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/837.751
CURRENT FILING DATE: 2001-04-18
PRIOR APPLICATION NUMBER: US 60/198,124
PRIOR FILING DATE: 2000-04-18
NUMBER OF SEQ ID NOS: 35
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/09837751 Patent No. US20020104124A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 27
LENGTH: 703
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                                                                                                                                                                                                                                                                                          APPLICANT: Liu, Qing
TITLE OF INVENTION: Method of Modifying the Content of Cottonseed Oil
FILE REFERENCE: 45-00
                                                                                                                                                                                                                                                                                                                            APPLICANT: Green, Allan APPLICANT: Singh, Surinder APPLICANT: Liu, Qing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: METHODS OF TREATMENT OF TYPE 2 DIABETES FILE REFERENCE: ARCD:307
CURRENT APPLICATION NUMBER: US/09/768,877
CURRENT FILING DATE: 2001-01-23
PRIOR APPLICATION NUMBER: 09/422,869
PRIOR FILING DATE: 1999-10-21
PRIOR FILING DATE: 1999-10-21
NUMBER OF SEQ ID NOS: 30
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189 WPMYLAFNVSGRYY 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 64.
                             3 WPSYLGYEKLGPYY 16
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OTANI, KENICHI
HANIS, CRAIG L.
BELL, GRAEME I.
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COX, NANCY J.
SREENAN, SEAMUS
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                                                            Conservative
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                                                                          45.5%;
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Pred. No.
                                                                          Score 45; DB Pred. No. 12;
                                                            Mismatches
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11;
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                                                                                       Length 385;
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US-09-794-960-5

Sequence 5, Application US/09794960

Patent No. US20020009774A1
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Best Local Similarity
~~+~hes 7; Conserva
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US-09-794-960-4
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SEQ ID NO 5
LENGTH: 300
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Matches
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                                                                                                                                                                                                                                  Sequence 4, Application US/09794960 Patent No. US20020009774A1
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SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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TITLE OF INVENTION: Recombinant Antibody Fragments as Autoantibody
TITLE OF INVENTION: Antagonists
FILE REFERENCE: SF01-025-2
CURRENT APPLICATION NUMBER: US/09/899,896
CURRENT FILING DATE: 2001-07-05
PRIOR APPLICATION NUMBER: 09/691,654
PRIOR APPLICATION NUMBER: 09/691,654
PRIOR FILING DATE: 2000-10-17
                                                      FILE REFERENCE: 35800/209290
CURRENT APPLICATION NUMBER: US/09/794,960
CURRENT FILING DATE: 2001-02-26
PRIOR APPLICATION NUMBER: US 60/185,333
PRIOR FILING DATE: 2000-02-28
                                                                                                                    APPLICANT: Kapeller-Libermann, Rosana
TITLE OF INVENTION: 18036, A No. US20020009774Alel Calpain-Like Protease
TITLE OF INVENTION: and Uses Thereof
FILE REFERENCE: 35800/20990774A166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Kapeller-Libermann, Rosana
TITLE OF INVENTION: 18036, A No. US20020009774A1el Calpain-Like Protease
TITLE OF INVENTION: and Uses Thereof
FILE REFERENCE: 35800/209290
CURRENT APPLICATION NUMBER: US/09/794,960
CURRENT FILING DATE: 2001-02-26
PRIOR APPLICATION NUMBER: US 60/185,333
PRIOR FILING DATE: 2000-02-28
SOFTWARE:
                                    NUMBER OF SEQ ID NOS:
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ORGANISM: human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: ProDom consensus sequence for calpain protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Artificial Sequence
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                    FastSEQ for Windows Version 4.0
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57.1%;
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Pred. No.
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; ORGANISM: Artificial Sequence; FEATURE: OTHER INFORMATION: PFAM consensus sequence for calpain family cystein; OTHER INFORMATION: protease US-09-794-960-4
                QΥ
                                                                                                           ; ORGANISM: Clostridium botulinum US-09-288-326-9
                                                                                                                                                                                                                                                                                                                                                                               RESULT 13
US-09-288-326-9
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US-09-852-399-4
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APPLICANT: Kei Roger Aoki
APPLICANT: George Sachs
TITLE OF INVENTION: Method and Compositions for the
TITLE OF INVENTION: Treatment of Pancreatitis
FILE REFERENCE: 17282
                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/288,326
CURRENT FILING DATE: 1999-04-08
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 9
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Matches
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                                                                            Query Match
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Patent No. US20020045232A1
                                               Best Local Similarity
Matches 8; Conserv
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CURRENT FILING DATE: 2001-05-09
PRIOR APPLICATION NUMBER: USSN 60/203,027
PRIOR FILING DATE: 2000-05-09
NUMBER OF SEQ ID NOS: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: PRODUCTION OF CONJUGATED LINOLEIC AND TITLE OF INVENTION: LINOLENIC ACIDS IN PLANTS FILE REFERENCE: BNZ-002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Qiu, Xiao
                                                                                                                                          LENGTH: 425
TYPE: PRT
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3 WPSYLGYEKLGPYY 16
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57.1%;
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Pred. No.
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Pred. No.
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230 WGDYLQYDK--PYY 241

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AGNOTH S.

ACANT: SREENAN, SEAMUS

APPLICANT: DHOU, YUN-PING

APPLICANT: HANIS, CRAIG L.

APPLICANT: HOVENTOO: METHODS OF TREATMENT OF TYPE 2 DIABETES

FILE REFERENCE: ARCD:307

CURRENT APPLICATION NUMBER: US/09/768,877

CURRENT APPLICATION NUMBER: 09/422,869

PRIOR APPLICATION NUMBER: 09/422,869

PRIOR FILING DATE: 1999-10-21

NUMBER OG SEQ ID NOS: 30

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 22

LENGTH: 714

TYPE: PRT

ORGANISM: Human

US-09-768-877-22

Query Mat*'

Best.
                                                                                                                                                                                                                           GEMERAL INC. USZUZULS GEMERAL INC. USZUZULS GEMERAL INC.

APPLICANT: Allergan, Inc.

APPLICANT: Acki, Kei Roger

APPLICANT: Steward, Lance E.

TITLE OF INVENTION: NEUROTOXINS WITH ENHANCED TARGET

TITLE OF INVENTION: SPECIFICITY

FILE REFERENCE: 36121-20002.00

CURRENT APPLICATION NUMBER: US/09/726,949A

CURRENT APPLICATION NUMBER: US/09/726,949A

CURRENT FILING DATE: 2000-11-29

NUMBER OF SEQ ID NOS: 1

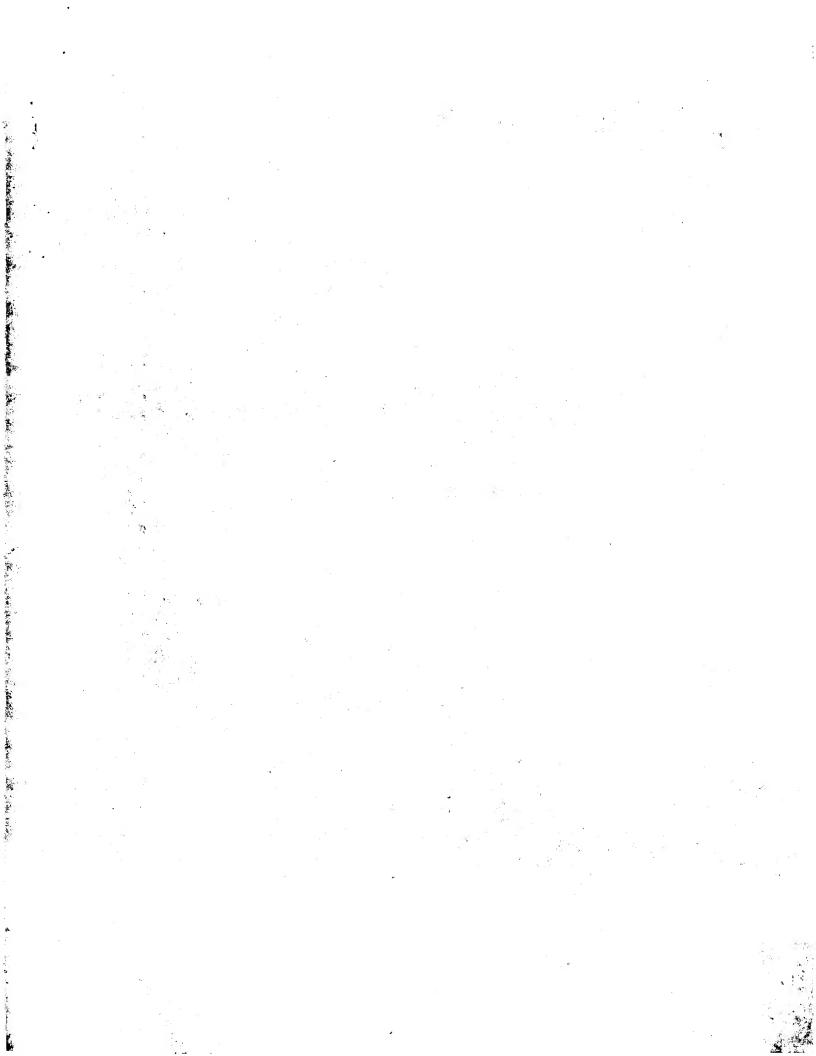
SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO 1

LENGTH: 1295

TYPE: PRT

ORGANISM: Clostridium botulinum
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Search completed: January 13, 2003, 14:35:26 Job time : 12 secs
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US-09-726-949A-1
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                                                                                                                                                    Query Match 42.4%;
Best Local Similarity 57.1%;
Matches 8; Conservative
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Best Local Similarity 57.1%;
Matches 8; Conservative
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62 PPVPQSLGYKDLGP 75
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Gapop 10.0 , Gapext 0.5
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Human interleukin-	AAB37797	21		51.5	5	œ
Human CANP used to	AAW19992	18		51.5	51	7
Novel human enzyme	AAU23305	22		51.5	51	١٥
Rat calpain 80kDa	AAB86130	22		52.5	52	
C-terminal peptide	AAY79064	21		90.9	90	4
Human protein sequ	AAB95633	22		100.0	99	. (
Phosphatase 1 prot	AAU02201	22		100.0	99	· K
Human protein phos	AAE14236	23	284	100.0	99	, _
Description	ID	BB	Query Match Length DB	Query	Score	Result

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599	514	385	708	708	712	703	703	703	486	429	399	392	300	466	466	443	443	283	283	223	219	127	27	26	21	21	21	1.9	19	19	82	720	518	462
22	22	22	23	23	18	23	23	18	21	21	22	21	22	20	19	21	21	22	22	15	15	11	12	12	23	21	18	23	21	18	23	23	23	23
AAY72375	AAU87301	42	AAU72885	AAE19179	AAW41565	AAU72884	AAE14338	AAW41564	AAG47097	AAG47098	AAM41149	AAG47099	AAM39363	AAY39899	AAW84355	AAY69555	AAB20512	AAB71733	AAB71730	AAR56236	AAR56235	AAR06355	AAR15273	AAR15276	ABG30389	AAB20596	AAW45498	ABG30388	AAB20595	AAW45497	ABP10799	ААМ49717	971	AAM49719
Amphiphilic recomb	Novel central nerv	Cotton oleoyl-PC d	73		calpain.	Human aspartyl pro	Human protease PRT	Human calpain. Ho	Arabidopsis thalia	Arabidopsis thalia	æ	Arabidopsis thalia	Human polypeptide	 T. thermophilus ph 		Talaromyces thermo	laromyces therm	phytase	_	166-111/112-65/h1-	h66-118/h13-65/11-	spon		0	Glycoprotein GpIIb	ein GPI	Ξ	lycoprote	in GPI	Targeting ligand d	ORFX prot	calpain	calpain	Murine calpain pro

ALIGNMENTS

AAE14236 ID AAE1 RESULT 1 Human protein phosphatase-1 (PP-1). 07-MAR-2002 AAE14236 standard; Protein; 284 (first entry)

Human; protein phosphatase-1; PP-1; gene therapy; tranquilliser; amnesia; arteriosclerosis; atherosclerosis; anxlety; anaemia; hepatitis; cataract; amyotrophic lateral sclerosis; adenocarcinoma; cerebral palsy; psoriasis; ulcerative colitis; myasthenia gravis; infection; schlzophrenic disorder; neurological disorder; epilepsy; neophasm; Alzheimer's disease; dementia; thyroiditis; dermatitis; diabetic mellitus; rheumatoid arthritis; stroke; granulomatous disease; haemolytic anaemia; crohn's disease; cancer; SCID; severe combined immunodeficiency disease; immune system disorder; trauma; developmental disorder; cell proliferative disorder; Addisease; systemic lupus erythematosus; Parkinson's disease; myelofibrosis; AIDS; leukaemia; antiinflammatory; cirrhosis; muscular dystrophy; allergy. WO200181590-A2 Homo sapiens.

20-APR-2000; 2000US-199010P 05-MAY-2000; 2000US-202340P 10-MAY-2000; 2000US-203424P

19-APR-2001; 2001WO-US12902

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      trauma, viral, bacterial, fungal, parasitic, protozoal and helminthic infections); neurological disorders (epilepsy, stroke, cerebral neoplasm, Alzheimer's disease, Huntington's disease, Parkinson's disease, amyotrophic lateral sclerosis, dementia, prion diseases); developmental disorders (Down syndrome, cerebral palsy, spinal cord diseases, amnesia, calizophrenic disorders, disorders, muscular dystrophy, anxiety, anaemia, schizophrenic disorders, disbetic neuropathy, Tourette's disorders (bursitis, arteriosclerosis, atherosclerosis, cirrhosis, hepatitis, myelofibrosis, psoriasis, cancers including adenocarcinoma, leukaemia, lymphoma, melanoma, myeloma, sarcoma and cancers of the bone, brain, breast, ovary, bladder, heart, kidney, liver, and pancreas. Protein phosphatases, its fragments and its antibodies are useful as elements on interactions, drug-target interactions and gene expression profiles. The present sequence is human protein phosphatase-1 (PP-1).
                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local
                                             Phosphatase 1; MEM1; therapeutic; diagnostic; MEM2; human; Alzheimer's disease; Parkinson's Disease; cancer; nephrology; female reproductive health; lung disorder; brean disorder; schizophr heart disorder; arrhythmia; muscular disorder; clotting deficiency; cobalamine deficiency; pernicious anaemia; diabetes; MEM4; MEM5; MEM
Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        autoimmune thyroiditis, atopic dermatitis, diabetic mellitus, rheumato arthritis, systemic lupus erythematosus, systemic sclerosis, Addison's disease, ulcerative colitis, haemodialysis uveitis, myasthenia gravis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           their corresponding DNA molecules. Protein phosphatases and their DNA's are useful for diagnosis, treatment and prevention of immune system disorders (AIDS, severe combined immunodeficiency disease (SCID), chronic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel polypeptides for diagnosing, preventing, treating immune system, neurological, developmental and cell proliferative disorders including cancer, comprises protein phosphatase polypeptides and encoding polypucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-MAY-2000; 2000US-205642P. 02-JUN-2000; 2000US-208854P.
                                                                                                                                                                                                                                                               AAU02201 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           granulomatous disease, autoimmune haemolytic anaemia, Crohn's disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim
                                  vision-related
                                                                                                                                                       Phosphatase 1
                                                                                                                                                                                            26-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      polynucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tang YT,
                                                                                                                                                                                                                                                                                                                                                       269 PEWPSYLGYEKLGPYY 284
                                                                                                                                                                                                                                                                                                    Ŋ
                                                                                                                                                                                                                                                                                                                                                                       1 PEWPSYLGYEKLGPYY 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NK,
                                                                                                                                                                                                                                                                                                                                                                                                                         16;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Stewart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              284
                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lee EA;
                                                                                                                                                     protein-like protein, MEM6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97-98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA;
                                  disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Khan FA,
rt EA, Tri
                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              to human protein phosphatases (PP-1 to PP-5) and WA molecules. Protein phosphatases and their DNA'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tribouley CM,
                                neoplastic
                                                                                                                                                                                                                                                                 285
                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 99;
Pred. No.
                                                                                                                                                                                                                                                                 B
                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                pathology; MEM7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patterson C,
Hafalia A,
                                                                                                                                                                                                                                                                                                                                                                                                                                     5.6e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 284;
                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nguyen DB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gandhi AR
                                                                                    schizophrenia;
                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      including
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                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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XEXTX

26-JUN-2001 AAB95633;

(first entry)

AAB95633 standard; Protein;

AΑ

0,

Human protein sequence SEQ ID NO:18363

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RESULT 3
AAB95633
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                                                                                                                                                                                                                                                                                                                            sequence relatedness, e.g., seven-pass transmembrane receptor protein (MEMI), glutamate receptor (MEM2-MEM4), pocassium channel protein (MEM5), oppossium channel protein (MEM5), and retinol-binding protein (MEM6). The MEM polypeptides (I), nucleic acids (II), and antibodies (III) are all useful for treating or preventing a pathology associated with (I) comprising administering (I), (II), or (III) to a subject (preferably a human). In addition, (I), (II), and (III) may be used to manufacture a medicament for treating a syndrome associated with a human disease that is associated with (I). Furthermore, (I) may be used to identify agents that bind to it, screen modulators of its activity and determine the presence or predisposition to a disease associated with altered levels of (II). Disorders for MEM1 include Alzheimer's or Parkinson's Disease.

(II) Disorders for MEM1 include Alzheimer's or Parkinson's Disease.

(II) Disorders for MEM1 include Alzheimer's or Parkinson's Disease.

(II) Disorders for MEM1 include Alzheimer's or Parkinson's Disease.

(III) MEM5, disorders include heart (arrhythmic disorders) and other muscular disorders include heart (arrhythmic disorders).
                                                                                                                                                  Matches
                                                                                                                                                                  Query Match
Best Local S
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27 - DEC - 1999;
27 - DEC - 1999;
29 - DEC - 1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel polypeptide comprising members of protein families seven-pass transmembrane receptor proteins) according to domains and sequence relatedness are useful for treating e.g., Alzheimer's and Parkinson's
                                                                                                                                                                                                                                                                            disorders, clotting deficiencies and cobalamine deficiencies (e.g., pernicious anaemia). Such disorders for MEM6 include diabetes, whereas disorders for MEM7 and MEM8 include vision-related disorders, cancer, \frac{1}{2}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The sequence represents the amino acid sequence of phosphatase 1 protein-like protein, MEM6, selected from a group (MEM1-MEM8) conmembers of protein families according to the presence of domains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             04-JAN-2000;
09-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Fig 27; 162pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB;
                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-398154/42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Spaderna
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14-DEC-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CURA-) CURAGEN CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-DEC-2000;
                                                                            270
                                                                                                                                                                Local
                                                                                                              1 PEWPSYLGYEKLGPYY 16
                                                                                                                                                                                                                                                             other neoplastic
                                                                            PEWPSYLGYEKLGPYY 285
                                                                                                                                                  l Similarity
16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SK,
                                                                                                                                                                                                                         285 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; 2000US-9966564.
; 2000US-0223929.
; 2000US-9966565.
                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000WO-US33909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Quinn KE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99US-0173165.
99US-0173362.
99US-0173544.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99US-0170564
                                                                                                                                                                                                                                                           pathologies
                                                                                                                                                                  100
                                                                                                                                                                    0.0%;
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                                                                                                                                                  0;:
                                                                                                                                                                  Score 99; I
Pred. No. 5
                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Muralidhara P,
                                                                                                                                                                                       DB 22;
                                                                                                                                                                    .6e-07;
                                                                                                                                                                                   Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Spytek KA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     presence of
or preventing,
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                                                                                                                                                  0;
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RESULT 4
AAY79064
ID AAY7
XX
AC AAY7
XX
DT 12-J
XX
DE C-te
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                                                                                                                                                                                                                                                                                                                                                                                              CC full-length cDNAs defined in the specification. Where a primer set to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprises a 5'-end CC sequence and an oligonucleotide comprises a 5'-end CC sequence and an oligonucleotide comprises a 5'-end sequence complementary to a coligonucleotide comprises a 3'-end sequence, where the CC oligonucleotide comprises a 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in CC the 5'-end sequence/3'-end sequence is selected from those defined in CC the specification. The primer sets can be used in antisense therapy and CC angles therapy. The primers are useful for synthesising polynucleotides, CC particularly full-length cDNAs. The primers are also useful for the CC detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length CDNAs easily without any specialised methods. AAH03166 to AAH1368 and CC AAB95893 represent human amino acid sequences; AAB92446 to CAB95893 represent human amino acid sequences; AAB92446 to CC of the present invention.
                                                                                                                                                                                                                                                                                                                                Query Match
Best Local :
                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-JUL-1999;
27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
09-JUN-2000;
C-terminal peptide of rat liver PP1 GL subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ota T,
                                            12-JUN-2000
                                                                                     AAY79064
                                                                                                                         AAY79064 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present full-length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ishii S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HELI-) HELIX RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-JUL-2000; 2000EP-0116126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-FEB-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human;
                                                                                                                                                                                                                              270 PEWPSYLGYEKLGPYY 285
                                                                                                                                                                                                                                                                      1 PEWPSYLGYEKLGPYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2001-318749/34.
                                                                                                                                                                                                                                                                                                               l Similarity
16; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Isogai T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sugiyama T,
                                                                                                                                                                                                                                                                                                                                                                                            285
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2000JP-0183767.
2000JP-0241899.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     invention
                                                                                                                                                                                                                                                                                                             Conservative
                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ID 18363;
                                                                                                                                                                                                                                                                                                                                                                                            AA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99JP-0300253
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                                                                                                                                                                                                                                                                                                                            100.0%;
                                                                                                                                                                                                                                                                      16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   describes primer sets for synthesising 5602
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                                                                                                                                                                                                                                                                                                        Score 99; DE
Pred. No. 5.6
0; Mismatches
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A, Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ROM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         English
                                                                                                                                                                                                                                                                                                                              DB 22;
5.6e-07;
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, Otsuki T;
                                                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                                                                                                 Length 285;
                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yamamoto
                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                        Gaps
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RESULT 5
AAB86130
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence represents the C-terminal amino acid sequence of the rat liver protein phosphatase I (PPI) glycogen targetting subunit (GL). The invention relates to the medicinal use of a compound capable of blocking the interaction of phosphorylase alpha with GL, where the compound comprises the present peptide sequence or a fragment of it. When phosphorylase alpha binds to GL it potently inhibits glycogen synthase phosphatase activity and inhibits glycogen synthesis, this contributes to high blood glucose levels. The invention also relates to a method for identifying the compound. The compound can be used to reduce the blood glucose level of a mammal, particularly a human, in hyperglycaemic disorders such as type I or type II diabetes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lowering blood sugar levels in the treatment of diabetes, us compound that blocks interaction between phosphorylase alpha protein phosphatase 1 glycogen-targetting subunit -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein phosphatase 1; PP1; glycogen targetting subunit; blood glucose; phosphorylase alpha; glycogen synthesis; hyperglycaemic disorder; GL; type I diabetes; type II diabetes.
                                              muscular; antitumor.
                                                                   structure-function study;
                                                                                      Ca-activated cystein
                                                                                                                Calpain;
                                                                                                                                                                                                                                                                                              AAB86130 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
Rattus norvegicus
                                                                                                                                                        Rat calpain 80kDa subdomain protein
                                                                                                                                                                                                    27-JUL-2001
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                                                                 calcium-activated cystein proteinase; human;
ated cystein proteinase; protein coordinate da
e-function study; ischemic condition; musculan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16
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                                                                                                                                                                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 90; Pred. No.
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                                                                                                                                                        fragment
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1;
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                                                                   muscular dystrophy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 16
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                                                                                    n; spatial structure; data; treatment;
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                                                                   tumor;
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13-DEC-2000; 2000EP-0127369

20-JUN-2001.

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RESULT 6
AAU23305
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31-JAN-2000;
04-FEB-2000;
24-FEB-2000;
02-MAR-2000;
16-MAR-2000;
17-MAR-2000;
18-PAR-2000;
19-MAY-2000;
07-JUN-2000;
28-JUN-2000;
30-JUN-2000;
30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      neutral calcium-activated cystein protease (calpain) family. The spatial structure (especially crystalline forms) are used for structure-function studies, particularly for identifying (pseudo)substrates, inhibitors and activators of calpains, potentially useful for treatment of ischemic conditions, muscular dystrophy and/or tumors. The products of the invention have anti-ischemic, muscular and antitumor activity. This sequence represents the rat calpain 80kba subunit described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (PLAC )
(PROT-)
                                                                                                                                                                                                                                                                                                                                       Human; oxidoreductase enzyme; transferase; hydrolase; lyase; isomerase ligase; hyperproliferative disorder; immunodeficiency disorder; autoimmune disorder; neurological disorder; metabolic disorder; inflammatory disorder; cardiovascular disorder; reproductive disorder;
                                                                                                                                                                                              17-JAN-2001;
                                                                                                                                                                                                                           02-AUG-2001
                                                                                                                                                                                                                                                        WO200155301-A2
                                                                                                                                                                                                                                                                                   Homo
                                                                                                                                                                                                                                                                                                               nephrotropic;
                                                                                                                                                                                                                                                                                                                            blood-related disorder; infectious disorder; cytostatic; anti arthritic;
                                                                                                                                                                                                                                                                                                                                                                                                                   Novel human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAU23305 standard; Protein; 144 AA.
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                                                                                                                                                                                                                                                                                  sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN PROTEROS BIOSTRUCTURES GMBH.
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2000US-0189874.
2000US-0190076.
2000US-0198123.
2000US-0205515.
2000US-020467.
2000US-0214886.
2000US-0215135.
2000US-0215136.
                                                                                                                   2000US-0179065.
2000US-0180628.
2000US-0184664.
2000US-0186350.
                                                                                                                                                                                                                                                                                                                                                                                                                 enzyme
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                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                              2001WO-US01239
                                                                                                                                                                                                                                                                                                               anticoagulant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99DE-1060225.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   containing calpain-derived polypeptides, useful for modulators and substrates, potentially useful e.
                                                                                                                                                                                                                                                                                                                                                                                                                polypeptide #391.
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60.0%;
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Pred. No. 18;
3; Mismatches
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   30-AUG-2000
31-SEP-2000
01-SEP-2000
01-SEP-2000
01-SEP-2000
01-SEP-2000
06-SEP-2000
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08-SEP-2000
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14-AUG-2000;
18-AUG-2000;
22-AUG-2000;
22-AUG-2000;
22-AUG-2000;
23-AUG-2000;
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14-AUG-2000;
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2000US-0218290.
2000US-0220963.
2000US-0224518.
2000US-0224518.
2000US-0225213.
2000US-0225214.
2000US-0225266.
2000US-0225266.
2000US-0225268.
2000US-0255277.
2000US-0225477.
2000US-0225477.
2000US-0225758.
2000US-0231968
2000US-0232397
2000US-0232399
2000US-0232400
2000US-0233063
2000US-0234274
2000US-0234274
2000US-0234274
2000US-0234297
2000US-0234997
2000US-0235834
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2000US-0235836
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2000US-0235836
2000US-0236369
2000US-0236369
2000US-0236369
2000US-023637
2000US-0236369
2000US-0237039
2000US-023937
2000US-023937
2000US-0239937
2000US-0239937
2000US-0231785
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2000US-0225759
2000US-0226681
2000US-0226686
2000US-0227182
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2000US-0229344
2000US-0229344
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2000US-0231413
2000US-0231244
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 \begin{matrix} G \cap G \cap G \cap G \cap G \times G \times G \\ G \cap G \cap G \cap G \end{matrix} 
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20-OCT 2000

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08-NOV 2000

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01-NO
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01-DEC-2000
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17-NOV-2000;
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17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
The present invention relates to the isolation of novel human enzyme polypeptides, and the cDNA (AAS40785-AAS41684) and genomic sequences encoding them. The enzyme polypeptides of the invention may comprise the functional classes of oxidoreductases, transferases, hydrolases, lyases, isomerases or ligases. The sequences of the invention are useful in the diagnosis, treatment, prevention and/or prognosis of a wide range of disorders including hyperproliferative disorders (e.g. cancer),
                                                                                                                                                                                                                          Novel polypeptides and polynucleotides useful for diagnosing, preventing, treating neural, immune system, muscular, reproductive, pulmonary, cardiovascular, renal, proliferative disorders and cance
                                                                                                                                                                       Claim 11;
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                                                                                                                                                                                                                                                                                                                                                                                                                       HUMAN
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2000US-0249216.
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2000US-0241826.
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2000US-0251868.
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2000US-0251479.
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2000US-0249299.
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2000US-0246611.
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2000US-0246477.
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2000US-0249244.
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2000US-0249212.
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2000US-0249210.
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2000US-0249207.
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2000US-0246609.
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2000US-0246527.
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2000US-0246523.
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                                                                                                                                                                  ID No 1301; 1180pp; English.
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cancerous

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Query Match

51 .5%;

Score

51;

DB 18;

Length 700

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RESULT 7
AAW19992
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Best Local :
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                        AAW19992 represents human calcium activated neutral protease (CANP). This protein was found to have an area of high homology with an interleukin-1 receptor (IL-1-R) intracellular ligand (encoded by cDNA clone 14w, see AAT71218) and thus will display some of the same properties of this protein. IL-1-R intracellular ligand proteins are used to screen for agents (e.g. antibodies) that are capable of inhibiting or blocking the binding of an IL-1-R intracellular ligand to the intracellular domain of IL-1-R, i.e. inhibitors of IL-1 activity. Such agents can be used to treat inflammatory conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        immunodeficiency disorders (e.g. AIDS) autoimmune disorders (e.g. arthritis), neurological disorders (e.g. Alzheimer's disease), metabolic disorders (e.g. phenylketonuria), inflammatory disorders (e.g. asthma), cardiovascular disorders (e.g. atherosclerosis), blood-related disorders (e.g. haemophilia), reproductive disorders (e.g. infertility) and infectious disorders (e.g. Influenza). The polynucleotides of the invention can also be used in gene therapy. ANU23915-AAU23814 represent the novel human enzyme polypeptides of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             invention.

Note: The sequence data for this patent did not specification, but was obtained in electronic fo at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
Sequence
                                                                                                                                                                           Claim 14; Page
                                                                                                                                                                                                                        Interleukin-1 receptor intracellular ligand proteins and related DNA used to identify inhibitors of the proteins for treatment of
                                                                                                                                                                                                                                                                    WPI; 1997-052315/05.
                                                                                                                                                                                                                                                                                                                                                           07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                        06-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
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                                                                                                                                                                                                                                                                                                                            (GEMY ) GENETICS INST INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            intracellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IL; interleukin; receptor; ligand; screening assay; inhibitor;
IL-1 mediated response; inflammation; inflammatory; antibody;
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domain; CANP;
ΑA;
                                                                                                                                                                            36-38; 54pp; English.
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60.0%;
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Pred. No.
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RESULT 8
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                                                                                                                                                                                                                                                                                                                                                      parasitic diseases, bacterial infections, sepsis, cachexia, autoimmune disorders, acute cardiovascular events, chronic myelogenous leukaemia a transplanted bone marrow-induced graft-versus-host disease, septic shoc immune complex-induced colitis, cerebrospinal fluid inflammation, multiple sclerosis, inflammatory responses associated with trauma, systemic inflammatory response syndrome (SIRS), adult respiratory distress syndrome (ARDS), acute liver failure, inflammatory bowel disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence is given in a specification relating to novel compositions and methods containing tetracycline or tetracycline-like compounds for treating and/or preventing acute inflammatory responses and diseases. Such diseases include acute inflammatory conditions associated with viral haemorrhagic diseases (including diseases caused by Bunyaviridea, Filoviridae, Filoviridae or Arenaviridae viruses),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel compositions comprising tetracycline or tetracycline-like compounds for the treatment and/or prevention of acute inflammatory responses and diseases, e.g. septic shock and immune complex-induced colitis -
                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 159-162; 183pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-679646/66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             multiple sclerosis; inflammatory bowel disease; Crohn's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         immunomodulator; cardiant; cytostatic; neuroprotective; respira
inflammation; infection; sepsis; cachexia; autoimmune disorder;
cardiovascular disorder; chronic myelogenous leukaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human interleukin-1 receptor intracellular ligand protein #4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-FEB-2001
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                                                                                       1 PEWPSYLGYEKLGPY 15
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                                                                                                                                                                                                                                                                                                                                Crohn's disease
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9; Conserv
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9; Conser
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AAB86128
ID AAB8
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Best Local
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                           screening; diagnosis
                                                                                                                   Murine capn12 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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This invention describes the novel spatial structure of human and rat neutral calcium-activated cystein protease (calpain) family. The spatial structure (especially crystalline forms) are used for structure-function studies, particularly for identifying (pseudo)substrates, inhibitors and activators of calpains, potentially useful for treatment of ischemic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Calpain; calcium-activated cystein proteinase; human; spatial structure; Ca-activated cystein proteinase; protein coordinate data; treatment; structure-function study; ischemic condition; muscular dystrophy; tumor;
Calpain protease; capn12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence represents the human calpain 80kDa subunit described
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             conditions, muscular dystrophy and/or tumors. The products of the invention have anti-ischemic, muscular and antitumor activity. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 15; Fig 4; 182pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Spatial structures containing calpain-derived polypeptides, useful for identifying calpain modulators and substrates, potentially useful e.g.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               method of the invention.
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Matches
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  2002-115441/16.
DB; ABA99770.
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DB; ABA99771.
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ng; diagnosis; capn12C.
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9; Conservative
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The calpain protease of the invention, related proteins and nucleic acid that encodes it, are useful for treatment (including gene therapy) of diseases associated with insufficient expression of the calpain protease. The protein is also used to screen for calpain protein effectors and to raise specific immunoglobulins (Ig) useful for diagnosis. Also the
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                                                                                                                                                                                        Claim 2;
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                                                                                                                                      This invention
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treating specific deficiency
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DB; ABA99769.
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9; Conservative
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                                                                                                                                    describes a novel murine calpain protease 12 (capn12).
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sis; capn12B.
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The present invention describes substantially purified human proteins (referred to as open reading frame, ORFX, where X is 1-11491 (see Table in the specification). ABN15762 to ABN27252 encode the human ORFX proteins given in ABP00010 to ABP11500. ORFX proteins are useful for treating or preventing a pathology associated with an ORFX-associated disorder in humans, and in the manufacture of a medicament for treating syndrome associated with ORFX-associated disorder. ORFX polynucleotide
                                                                                                                                                                                      lupus erythematosus, hypertension, hypothyroidism, cholesterol ester storage disease, various immune deficiencies and disorders, infectious diseases, autoimmune disorders such as multiple sclerosis, rheumatoid arthritis, autoimmune thyroiditis, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. ORFX proteins are also useful for treating burns, incisions, ulcers, for treating osteoporosis,
                                                                                                                                                                                                                                                                                                               sequences can be used in gene therapy. ORFX sequences can be used in the treatment of cancer, hyperproliferative disorders, cirrhosis of liver, psoriasis, benign tumours, keloid, degenerative disorders, haemorrhage, osteoarthritis, neurodegenerative disorders, disorders related to organ transplantation, cardiovascular diseases, diabetes mellitus, systemic transplantation, cardiovascular diseases, diabetes mellitus, systemic transplantation, cardiovascular diseases, diabetes mellitus, systemic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hyperproliferative disorder; psoriasis; benign tumour; haemorrhage; degenerative disorder; osteoarthritis; neurodegenerative disorder; cardiovascular disease; diabetes mellitus; systemic lupus erythematosus; hypertension; hypothyroidism; cholesterol ester storage disease; hypertension; hypothyroidism; cholesterol ester storage disease;
                                     N.B. The sequence data for this patent did not specification, but was obtained in electronic for at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                           bone degenerative disorders, or periodontal disease, and for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues and conditions resulting from
  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and autoimmune disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            myasthenia gravis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABP10799;
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                                                                                                           systemic cytokine damage.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-MAY-2000;
29-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human ORFX protein sequence SEQ ID NO:21580.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mmune deficiency; immune disorder; infectious disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2002-106308/14.
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    82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID 21580;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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2000US-228716P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2001WO-US10836
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1037pp; English.
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psoriasis; benign tumour;
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                                                                 format
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                                                                                   torm
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directly from WIPO
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Query Match Best Local Similarity

49.0%; 60.0%;

Score Pred.

48.5; DB 23; No. 6;

Length 82

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The present sequence represents a targeting ligand directed to the CC GPIIbIIIa receptor. The invention relates to a contrast agent for CC diagnostic imaging or a target composition which comprises: (i) a lipid, CC protein or polymer and (ii) a gas, in combination with (iii) a targeting CC ligand (T1). Tl targets cells or receptors selected from myocardial, CC endothelial, epithelial and tumour cells and the glycoprotein GPIIb/IIIa CC receptor. Also claimed are: a composition comprising vesicles containing CC (i) - (iii) and an aqueous carrier; a targeted vesicle composition CC comprising a fluorinated gas and a targeting ligand (T1) which targets tissues or receptors; a formulation for therapeutic or diagnostic use comprising (i) (iii) and a bioactive agent; and a method for providing an internal region of a patient, or for diagnosing the presence CC of diseased tissue, comprising: (a) administration of a composition as above; and (b) scanning the patient using ultrasound to obtain a visible cuseful for imaging or diagnosing the presence of diseased tissue. The methods and compounds are cuseful for imaging or diagnosing the presence of diseased tissue but also CC gastrointestinal and cardiovascular regions. In particular the ligand CC targets regions of arteriosclerosis. Stabilised vesicles are used to deliver active agents to an intended target such as tissue or a
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AAW45497
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Matches 8; Conserv
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                                                                       Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-1996;
07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         glycoprotein GPIIb/IIIa receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Targeting ligand directed to the glycoprotein GPIIb/IIIa receptor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW45497 standard; peptide;
                                                                                                    receptor, and ultrasound can then be used to promote rupture of the vesicles and release a bioactive or diagnostic agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Pages 55-56; 175pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1997-077233/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Shen D, Unger EC,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-JUN-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contrast agent; targeted composition; diagnosis; diseased tissue;
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95US-0497684.
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Score 48; DB 18; Length 19; Pred. No. 1.5; 1; Mismatches 4; Indels
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        Pred. No. is the number of results predicted by chance to I score greater than or equal to the score of the result being and is derived by analysis of the total score distribution
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          protein search, using sw model
      Query
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1: /cgn2_6/ptcdata/2/paa/PcT_NEW_COMB.pep:*

2: /cgn2_6/ptcdata/2/paa/US06_NEW_COMB.pep:*

3: /cgn2_6/ptcdata/2/paa/US08_NEW_COMB.pep:*

4: /cgn2_6/ptcdata/2/paa/US08_NEW_COMB.pep:*

5: /cgn2_6/ptcdata/2/paa/US08_NEW_COMB.pep:*

6: /cgn2_6/ptcdata/2/paa/US08_NEW_COMB.pep:*

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US-09-884-319-7
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Compugen Ltd.
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Query Match Best Local s Matches 16 Matches 16 y 1 PEWF j b 269 PEWF	SSULT 1 SEQUENCE (1 Applicate GENERAL INFORMATION: APPLICANT: TANG, Y APPLICANT: YUE, HE APPLICANT: WANG, Y APPLICANT: STEWART APPLICANT: HAFALIA APPLICANT: LEE, ET TITLE OF INVENTION: FILE REFERENCE: PICURRENT FILING DATE PRIOR APPLICATION OF SEQ ID NO SOFTWARE: PERL PICURE: PICURGE:	27 27 28 33 33 33 33 33 33 33 33 33 34 34 34 34
ch 16; 16; 11111	74-1 NFORMAN NFORMAN T: INC: T: INC: T: YUI T: YUI T: WAH	4444444444444
tch al Similarity al Similarity bewpsylgyeklgpyy fill pewpsylgyeklgpyy	JUT 1 OLO-258-274-1 Quence 1, Application US/10258274 SMERAL INFORMATION: APPLICANT: INCYTE GENOMICS, INC. APPLICANT: TANG, Y. Tom APPLICANT: YUE, Henry APPLICANT: KHAN, Farrah APPLICANT: KHAN, Farrah APPLICANT: GANDHI, Ameena R. APPLICANT: STEWARP, A. Elizabeth APPLICANT: HAFALIA, NATINDER APPLICANT: HAFALIA, April APPLICANT: ELLIOTT, Vicki S. APPLICANT: LEE, Ernestine Hee PITLE OF INVENTION: PROTEIN PHOSPHI FILE REFERENCE: PI-0077 PCT FURRENT FILING DATE: 2000-04-20; 2000 UMBER OF SEQ ID NOS: 10 SOFIMARE: PRT ORGANISM: Homo Sapiens FEATURE: misc_feature OTHER INFORMATION: Incyte ID NO: 4 OTHER INFORMATION: Incyte ID NO: 4 OTHER INFORMATION: Incyte ID NO: 4	4004 4004 4004 4004 4004 4004 4004 400
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0%;	INC INC Zabe Erin PHO US/ 10-71 10-71 10-71 10-71 10-71 10-71 10-71	5 1 2 3 3 5 5 5 7 5 5 5 5 5 5 5 5 5 5 5 5 5 5
Score 99; DB 6; Length 2; Pred. No. 8.9e-08; 0; Mismatches 0; Indels	TASES 58,274 10; 60/202,340; 60/20 1-05-05; 2000-05-10;	US-09-308-345A-47 US-10-276-774-2387 PCT-USO2-32727-3579 US-01-057-498-3579 US-09-724-676-81226 US-09-724-676-81225 US-09-724-676-81234 US-09-724-676-81234 US-09-724-676-81224 PCT-USO2-32727-23614 US-10-276-794-1184 US-10-276-774-1184 US-09-134-000C-6536 US-09-324-676-33 PCT-USO2-32850-14 US-09-324-676-73148 US-09-724-676-73148
284; 1s 0;	3,424; 60/205,642; 60/ 2000-05-18; 2000-06-02	Sequence
Gaps	05,642; 2000-0	47, Appl 2387, Ap 3579, Ap 81226, A 81225, A 81225, A 81224, A 81224, A 81224, A 81224, A 81224, A 812361, A 812361, A 8124, A
0;	60/208,8 6-02	\$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$

RESULT 2
US-09-308-345A-46
; Sequence 46, Application US/09308345A
; GENERAL INFORMATION:
; APPLICANT: BOEHM, Thomas;

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NUMBER OF SEQ ID NOS: 49
SOFTWARE: WORDPERFECT v. 6.1
SEQ ID NO 46
LENGTH: 700
TYPE: PRT
ORGANISM: mouse
US-09-308-345A-46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 81229, Application US/09724676

GENERAL INFORMATION:
APPLICANT: Compugen LTD
ITILE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTMARE: Patentin version 3.2
SEQ ID NO 81229
LENGTH: 395
TYPE: PRT
                                                                                                                                                                           Sequence 81229, Application US/09724676A

GENERAL INFORMATION:
APPLICANT: Compugen LTD

TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A

CURRENT FILING DATE: 2000-11-28

NUMBER OF SEQ ID NOS: 97222

SOFTWARE: Patentin version 3.2

SEQ ID NO 81229

LENGTH: 395
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                                                                                                                            ; TYPE: PRT ; ORGANISM: Homo sapiens US-09-724-676A-81229
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Homo sapiens 
US-09-724-676-81229
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Best Local :
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Best Local Similarity
                                                                Matches
                                                                               Query Match
Best Local (
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nes 9; Conserv
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94 PAIPSALGFKELGPY 108
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                               PEWPSYLGYEKLGPY 15
 PAIPSALGFKELGPY 108
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                                                                Conservative
                                                                               51.5%;
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66.7%;
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Pred. No. 2.9;
                                                                               Score 51; I
Pred. No. 2.
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                                                                               DB 5;
2.9;
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US-09-724-676-81228
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US-09-724-676A-81228
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APPLICANT: Compugen LTD

TITLE OF INVENTION: Variants of alternative splicing

FILE REFERENCE: 129181.4 Compugen

CURRENT APPLICATION NUMBER: US/09/724,676A

CURRENT FILING DATE: 2000-11-28

NUMBER OF SEQ ID NOS: 97222

SOPTWARE: PatentIn version 3.2

SEQ ID NO 81228

LENGTH: 594
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SEQ ID NO 81228
LENGTH: 594
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GENERAL INFORMATION
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Best Local
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CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
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TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 12918.4 Compugen
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ORGANISM: Homo sapiens
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Local Similarity 60.0%;
tes 9; Conservative
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COUNTRY: USA
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: LEGAL AFFAIRS, GENESTREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                               APPLICANT: Lin, Lih-Ling
Graham, James
                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                TITLE OF INVENTION: NOVEL INTERLEUKIN-1 RECEPTOR
                                                                                      CITY: Cambridge
STATE: MA
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Pred. No. 4
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                                                                                                                                        GENETICS INSTITUTE, INC
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US-09-884-319A-7; Sequence 7, Application US/09884319A; GENERAL INFORMATION:
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Best Local Similarity
Matches 9; Conserv
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                                                          COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/09/884,319A
FILING DATE: 18-Jun-2001
CLASSIFICATION INDER: US/09/884,319A
FILING DATE: 18-Jun-2001
PRIOR APPLICATION NUMBER: US/09/083,516
FILING DATE: <Unknown>
APPLICATION NUMBER: US/09/083,516
FILING DATE: <Unknown>
APPLICATION UMBER: US/09/083,516
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
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REFERENCE/DOCKET NUMBER: G15258
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: LEGAL AFFAIRS, GENETICS INSTITUTE, INC
STREET: 87 CambridgePark Drive
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FILING DATE: 18-Jun-2001
CLASSIFICATION: CUNKNOWN>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: NOVEL INTERLEUKIN-1 RECEPTOR
INTERCELLULAR LIGAND PROTEINS AND INHIBITORS OF LIGAND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Lin, Lih-Ling
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FILING DATE: <Unknown>
APPLICATION NUMBER: 08/487,942
FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Cambridge
STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
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SOFTWARE: PatentIn Release #1.0, Version #1.25
                      NAME: Brown, Scott A. REGISTRATION NUMBER: 32,724
                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 02140
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TELEFAX: (617) 876-5851
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REFERENCE/DOCKET NUMBER: GI5258
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RESULT 10

US-09-724-676-81227

Sequence 81227, Application US/09724676

GENERAL INFORMATION:

APPLICANT: Compugen LTD

TITLE OF INVENTION: Variants of alternative splicing

FILE REFERENCE: 129181.4 Compugen

CURRENT APPLICATION NUMBER: US/09/724,676

CURRENT FILING DATE: 2000-11-28

NUMBER OF SEQ ID NOS: 97222

SOFTMARE: PatentIn version 3.2

SEQ ID NO 81227

LENGTH: 754
                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Homo sapiens US-10-293-017-78
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Best Local :
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APPLICANT:
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Matches 9; Conserv
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TELEPHONE: (617) 498-8224
TELEPAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 700 maino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Wieloch, Tadeusz
APPLICANT: Gonzalez-Zulueta, Mirella
TITLE OF INVENTION: Regulated Genes in the Pathophysiology of Ischemic Stroke
FILE REFERENCE: AGYT-007US1
CURRENT APPLICATION NUMBER: US/10/293,017
CURRENT FILING DATE: 2002-11-12
PRIOR APPLICATION NUMBER: 60/384,522
PRIOR APPLICATION NUMBER: 60/384,522
PRIOR PILING DATE: 2002-05-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 60/338,296 PRIOR FILING DATE: 2001-11-09 NUMBER OF SEQ ID NOS: 86
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APPLICANT: Chin, D:
APPLICANT: Von Sch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
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Von Schack, David
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Pred. No. 5;
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Pred. No. 5;
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RESULT 11
US-09-724-676A-81227
; Sequence 81227, Application US/09724676A
; GENERAL INFORMATION:
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; Sequence 12, Application US/09813484
; GENERAL INFORMATION:
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                                           RESULT 13
US-09-813-484-13
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Sequence 13, Application US/09813484 GENERAL INFORMATION:
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TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
SEQ ID NO 81227
LENGTH: 754
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Best Local Similarity 60.0
Matches 9; Conservative
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Best Local
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TITLE OF INVENTION: Novel Methods Of Ultrasound Treatment Using Gas Or Gaseous Precui
TITLE OF INVENTION: Filled Compositions
FILE REFERENCE: UNGR1600

CURRENT APPLICATION NUMBER: US/09/813,484

CURRENT FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 08/929,847

PRIOR APPLICATION NUMBER: 08/929,847

PRIOR FILING DATE: 1997-09-15

NUMBER OF SEO ID NOS: 39

COURTURED SECOND NOS: 39
                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                  FEATURE:
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                                                                                                                                                                    48.5%;
Local Similarity 61.5%;
les 8; Conservative
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Pred. No. 0.48;
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Pred. No. 5.4;
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RESULT 14
US-09-635-504-31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 31, Application US/09635504
GENERAL INFORMATION:
APPLICANT: Van Loon, Adolphus
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CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 08/929,847
PRIOR FILING DATE: 1997-09-15
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TYPE: PRT
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TITLE OF INVENTION: Novel Methods Of Ultrasound Treatment Using Gas Or Gaseous Pre
TITLE OF INVENTION: Filled Compositions
FILE REFERENCE: UNGR1600
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                                                                                                                                                       TELEPHONE: (201) 235-2:
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
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les 8; Conserv
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/744,231
FILING DATE: <Unknown>
APPLICATION NUMBER: 08/424,757
FILING DATE: 18-APR-195
ATTORNEY/AGENT INFORMATION:
                                                          MOLECULE TYPE: protein FEATURE:
                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 07110
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mitchell, David
TITLE OF INVENTION: POLYPEPTIDES WITH PHYTASE ACTIVITY
NUMBER OF SEQUENCES: 35
                  NAME/KEY:
                                                                                               LENGTH: 466 amino acids TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/09/635,504 FILING DATE: 09-Aug-2000
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  OTHER INFORMATION:
                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: Case Docket 9339
                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 32142
                                                                                                                                                                                                                                                                                                    NAME: Kass, Alan P
                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: <Unknown>
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                    misc_feature
204
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/note="potential N-glycosylation site"
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RESULT 15
US-09-308-345A-49
Sequence 49, Application US/09308345A
GENERAL INFORMATION:
APPLICANT: BOEHM, Thomas;
APPLICANT: DEAR, Neil T:
APPLICANT: DEAR, Neil T:
FILE OF INVENTION: NOVel calpains, their preparation and use FILE REFERENCE: 0050/47576
CURRENT APPLICATION NUMBER: US/09/308,345A
CURRENT FILING DATE: 1999-05-19
NUMBER OF SEQ ID NOS: 49
SOFTWARE: WordPerfect v. 6.1
SEQ ID NO 49
LENGTH: 703
TYPE: PRT
ORGANISM: rat
US-09-308-345A-49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature;
LOCATION: 372
OTHER INFORMATION: /note="potential N-glycosylation site";
SEQUENCE DESCRIPTION: SEQ ID NO: 31:
US-09-635-504-31
Search completed: January 13, 2003, 14:35:47 Job time: 15 secs
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Best Local Similarity 53.3%;
Matches 8; Conservative
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Best Local Similarity 64.3%;
Matches 9; Conservative
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285 EWQAYDYYQSLGKYY 299
                                                                       1 PEWPSYLGYEKLGP 14
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52 PACPSALGYKDLGP 65
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LOCATION: 269
OTHER INFORMATION: /note="potential N-glycosylation site"
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LOCATION: 348
COTHER INFORMATION: /note="potential N-glycosylation site"
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LOCATION: 335
OTHER INFORMATION: /note="potential N-glycosylation site"
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Maximum DB
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Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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length: 2000000000
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Listing first 45 summaries
                                                                                                : //cgn2_6/ptodata/1/paa/US08_COMB.pep: *
:/cgn2_6/ptodata/1/paa/US06_COMB.pep: *
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:/cgn2_6/ptodata/1/paa/US08_COMB.pep: *
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ALIGNMENTS

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; ORGANISM: Rattus
US-09-763-848-1
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                                                                                                                                                            PRIOR APPLICATION NUMBER: GB 9818650.5
PRIOR FILING DATE: 1998-08-27
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
LENGTH: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Applicat
GENERAL INFORMATION:
  Matches
                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                APPLICANT: Cohen, Patricia T.W.
APPLICANT: Cohen, Patricia T.W.
APPLICANT: Armstrong, Christopher G.
APPLICANT: Doherty, Martin J.
APPLICANT: Doherty, Martin J.
TITLE OF INVENTION: Subunit of Protein Phosphatase 1 and Methods of Making
TITLE OF INVENTION: and Using The Same
FILE REFERENCE: 002.00140
CURRENT APPLICATION NUMBER: US/09/763,848
CURRENT FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: PCT/GB99/02761
PRIOR FILING DATE: 1999-08-19
PRIOR FILING DATE: 1999-08-19
                                                                                                                                        LENGTH: 16
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Application US/09763848
  Conservative
                      100.0%; Score 99; DB 21; 100.0%; Pred. No. 1.1e-07;
  0;
  Mismatches
                                            Length 16;
  Indels
0
Gaps
0
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Result No.

Score

Match Length

DB

B

Description

66 66 66 66 66

100.0 100.0 100.0 100.0 100.0

16 162 282 284 284 284

US-09-763-848-1 US-60-169-867-4624 US-09-737-149-43 US-09-300-327-3 US-09-737-149-42 US-60-199-010-1

Sequence 1, Appli Sequence 4624, Ap Sequence 43, Appli Sequence 3, Appli Sequence 42, Appli Sequence 1, Appli

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RESULT 2
US-60-169-867-4624
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US-09-737-149-43
                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 60/170,564
PRIOR FILING DATE: 1999-12-14
PRIOR APPLICATION NUMBER: 60/173,165
PRIOR TILING DATE: 1999-12-27
PRIOR APPLICATION NUMBER: 60/173,362
PRIOR FILING DATE: 1999-12-27
PRIOR FILING DATE: 1999-12-27
PRIOR APPLICATION NUMBER: 60/173,544
PRIOR FILING DATE: 1999-12-29
PRIOR FILING DATE: 1999-12-29
PRIOR APPLICATION NUMBER: 60/174,404
PRIOR FILING DATE: 2000-01-04
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GENERAL INFORMATION:

APPLICANT: BONAZZI, VIVIEN

TITLE OF INVENTION: ISOLATED HUMAN DRUG TARGET PROTEINS,

TITLE OF INVENTION: AUCLEIC ACID MOLECULES ENCODING HUMAN DRUG TARGET PROTEINS,

TITLE OF INVENTION: AND USES THEREOF

FILE REFERENCE: CL000160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 16; Conservative 0
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LENGTH: 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                            SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 43, Application US/09737149
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CURRENT FILLNG DATE: 1999-12-09
NUMBER OF SEQ ID NOS: 8230
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                               PRIOR FILING DATE: 2000-08-09
NUMBER OF SEQ ID NOS: 49
                                                                                                                                                                                                                                                                                                                                                PRIOR FILING DATE: PRIOR APPLICATION |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/737,149
CURRENT FILING DATE: 2001-06-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Muralidhara, Padigaru
APPLICANT: Spytek, Kimberly A.
TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same
FILE REFERENCE: 15966-620 CIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Spaderna, Steven K APPLICANT: Quinn, Kerry E.
                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 60/174,962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Human
                    OTHER INFORMATION: Consensus Sequence

NAME/KEY: VARIANT

LOCATION: (1)..(282)

OTHER INFORMATION: where x is a residue at which the query and

OTHER INFORMATION: subject seugnces are not identical.
                                                                                                                                                                     ORGANISM: Artificial Sequence
                                                                                                                                                                                                    TYPE: PRT
                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                        LENGTH: 282
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                                                                                                                                                                                                                                                                                                                                             FILING DATE: 2000-01-07
APPLICATION NUMBER: 60/223,929
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Pred. No. 1.2e-06;
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Matches
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Best Local Similarity
Matches 16; Conserv
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LENGTH: 284
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APPLICANT: Cohen, Patricia T
APPLICANT: Cohen, Phillip
APPLICANT: Young, Peter R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 42, Application US/09737149 GENERAL INFORMATION:
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              SOFTWARE: PatentIn Ver.
SEQ ID NO 42
LENGTH: 284
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: A PROTEIN PHOSPHATASE 1 BINDING PROTEIN, R5 FILE REFERENCE: ATG-50033-1 CURRENT APPLICATION NUMBER: US/09/300,327 CURRENT FILING DATE: 1999-04-27 EARLIER APPLICATION NUMBER: 08/767,096 EARLIER FILING DATE: 1996-12-05 NUMBER OF SEQ ID NOS: 6
                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Spytek, Kimberly Å.
TITLE OF INVENTION: Polypeptides and Nucleic Acids
FILE REFERENCE: 15966-520 CIP
CURRENT APPLICATION NUMBER: US/09/737,149
CURRENT FILING DATE: 2001-06-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Spaderna, Steven K APPLICANT: Quinn, Kerry E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Ver. 2.0
                                                                                                                            PRIOR FILING DATE: 2000-01-04
PRIOR APPLICATION NUMBER: 60/174,962
PRIOR FILING DATE: 2000-01-07
PRIOR APPLICATION NUMBER: 60/223,929
                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 60/173,544
PRIOR FILING DATE: 1999-12-29
PRIOR APPLICATION NUMBER: 60/174,404
                                                                                                                                                                                                                                                                  PRIOR FILING DATE: 1999-12-27
PRIOR APPLICATION NUMBER: 60/173,362
PRIOR FILING DATE: 1999-12-27
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                                                                                            NUMBER OF SEQ ID NOS: 49
                                                                                                                PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 60/173,165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
ORGANISM: Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 PEWPSYLGYEKLGPYY 16
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| 269 PEWPSYLGYEKLGPYY 284
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Pred. No. 2.1e-06;
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CURRENT APPLICATION NUMBER: US/09/629,469A
CURRENT FILING DATE: 2000-07-28
PRIOR APPLICATION NUMBER: JP 1999-248036
PRIOR ETLING DATE: 1999-07-29
PRIOR APPLICATION NUMBER: JP 1999-300253
PRIOR APPLICATION NUMBER: JP 2000-118776
PRIOR APPLICATION NUMBER: JP 2000-183767
PRIOR FILING DATE: 2000-01-11
PRIOR APPLICATION NUMBER: JP 2000-183767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-629-469A-18363
; Sequence 18363, Application US/09629469A
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CURRENT FILING DATE: 2000-04-20
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PERL Program
SEO ID NO 1
SEO ID NO 1
LENGTH: 284
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/60199010 GENERAL INFORMATION:
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                APPLICANT: SUGIYAMA, TOMOYASU
APPLICANT: WAKAWATSU, AI
APPLICANT: NAGAI, KEIICHI
APPLICANT: OTSUKI, TETSUJI
TITLE OF INVENTION: PRIMERS FOR SYNTHESIZING FULL-LENGTH CDNA AND THEIR USE
FILE REFERENCE: 084335/0123
                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Tang, Y.Tom
APPLICANT: Yue, Henry
APPLICANT: Khan, Farrah A.
APPLICANT: Wang, Yu-mei Eureka
APPLICANT: Wang, Yu-mei Chandra
APPLICANT: Patterson, Chandra
TITLE OF INVENTION: PROTEIN PHOSPHATASES
FILE REFERENCE: PI-0077 P
                                                                                                                                                                                                                                                                                                          APPLICANT:
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                  APPLICATION NUMBER: JP 2000-241899
                                     FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                            NISHIKAWA, TEX
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SAITO, KAORU
                                                                                                                                                                                                                                                                                                                           ISHII, SHIZUKO
                                                                                                                                                                                                                                                                                                                                            YAMAMOTO, JUNICHI
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2000-06-09
                                   2000-05-02
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100.0%; Pred. No. 2
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Pred. No.
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US-09-791-537-99714; Sequence 99714, Application; GENERAL INFORMATION: APPLICANT: Bionomix, Inc.
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US-09-737-149-12
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                                                                                                                                                                               RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/99/737,149
CURRENT ELLING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/170,564
PRIOR FILING DATE: 1999-12-14
PRIOR APPLICATION NUMBER: 60/173,165
PRIOR APPLICATION NUMBER: 60/173,362
PRIOR FILING DATE: 1999-12-27
PRIOR APPLICATION NUMBER: 60/173,362
PRIOR FILING DATE: 1999-12-27
PRIOR APPLICATION NUMBER: 60/173,544
PRIOR FILING DATE: 1999-12-29
PRIOR APPLICATION NUMBER: 60/174,404
PRIOR FILING DATE: 1999-12-29
PRIOR APPLICATION NUMBER: 60/174,962
PRIOR APPLICATION NUMBER: 60/223,929
PRIOR APPLICATION NUMBER: 60/223,929
PRIOR FILING DATE: 2000-01-07
PRIOR APPLICATION NUMBER: 60/223,929
PRIOR FILING DATE: 2000-01-07
PRIOR APPLICATION NUMBER: 60/223,929
PRIOR FILING DATE: 2000-08-09
                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 16; Conserv
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SEQ ID NO 12
LENGTH: 285
TYPE: PRT
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PRIOR FILING DATE: 2000-07-17
NUMBER OF SEQ ID NOS: 19025
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 18363
LENGTH: 285
TYPE: PRT
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APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Spaderna, Steven K
APPLICANT: Ouinn, Kerry E.
APPLICANT: Shimkets, Richard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Muralidhara, Padigaru
APPLICANT: Spytek, Kimberly A.
TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same
FILE REFERENCE: 15966-620 CIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 60/159,590 PRIOR FILING DATE: 1999-10-18
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                                                                                                                                                                                                                                                    270 PEWPSYLGYEKLGPYY 285
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cal Similarity 100.0%;
16; Conservation
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                                                                                                                                US/09791537
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....LUCANT: Danzer, Joseph
FITTLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 122174
LENGTH: 700
TYPE: PPT
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FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PatentIn version 3.0
SEQ ID NO 99714
LENGTH: 700
TYPE: PRT
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US-09-791-537-99714
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US-09-791-537-131857
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                                                                           US-09-791-537-131857
                                                                                                      SOFTWARE: PatentIn version 3.0
SEQ ID NO 131857
LENCTH: 700
TYPE: PRT
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Best Local Similarity
                           Query Match
Best Local
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Best Local Similarity
              Matches
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APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
APPLICANT: Debe, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ 1D NOS: 153055
                                                                                       ORGANISM: Mus musculus
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                            Similarity
Conservative
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66.7%;
           Score 56; DB Pred. No. 19; 2; Mismatches
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Pred. No.
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Pred. No.
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19;
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19;
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                           APPLICANT:
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; SEQ ID NO 12
; LENGTH: 700
; TYPE: PRT
; ORCANISM: Homo sapiens
US-60-350-064-12
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US-60-350-064-12
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Best Local Similarity
""" Conserv
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US-10-155-881-31730
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                                                                                                          US-10-219-999-49589
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GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL CYSTEINE PROTEASE (
TITLE OF INVENTION: SUPERFAMILY, Protease-43
FILE REFERENCE: D0220 PSP
CURRENT APPLICATION NUMBER: US/50/350,064
CURRENT FILING DATE: 2002-01-18
NUMBER OF SEQ ID NOS: 103
                Sequence 49589, Application US/10219999
GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Edgerton, Michael D
APPLICANT: Hinkle, Gregory J.
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SEQ ID NO 31730
LENGTH: 359
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CURRENT FILING DATE: 2002-05-22
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                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52
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Edgerton, Michael D
Hinkle, Gregory J.
Kovalic, David K.
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Pred. No.
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Pred. No.
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40;
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Liu, Jingdong

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RESULT 15
US-60-324-109-27547
US-60-324-109-27547
Sequence 27547, Application US/60324109
GENERAL INFORMATION:
APPLICANT: CaO, Yongwei
APPLICANT: Edgerton, Michael D
APPLICANT: Hinkle, Gregory J
APPLICANT: Kovalic, David K.
APPLICANT: Kovalic, David K.
APPLICANT: Stein, Jusquang
APPLICANT: Stein, Jusquang
CURRENT FILING CDNA SEQUENCES AND USES FOR PLANT IMPROVEMENT
FILE REFERENCE: 38-0(52726)8
CURRENT APPLICATION NUMBER: US/60/324,109
CURRENT FILING DATE: 2001-09-21
NUMBER OF SEQ ID NOS: 33196
SEQ ID NO 27547
LENGTH: 359
TYPE: PRT
CRANISM: Zea mays
FEATURE:
US-60-324-109-27547
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CURRENT APPLICATION NUMBER: US/10/219,999
CURRENT FILLING DATE: 2002-08-15
PRIOR APPLICATION NUMBER: US 60/324,109
PRIOR FILLING DATE: 2001-09-21
PRIOR APPLICATION NUMBER: US 60/312,544
PRIOR APPLICATION NUMBER: US 60/312,544
PRIOR FILLING DATE: 2001-09-21
PRIOR FILLING DATE: 2001-08-15
NUMBER OF SEQ ID NOS: 63520
SEQ ID NO 49589
LENGTH: 359
TYPE: PRT
ORGANISM: Zea mays
US-10-219-999-49589
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Search completed: January 13, 2003, 14:38:15 Job time: 141 secs
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                                                                                                                                                          Query Match 52.5%;
Best Local Similarity 46.7%;
Matches 7; Conservative
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Best Local Similarity 46.7%;
Matches 7; Conservative
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Pred. No. 40;
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                                                                                                                                                            Mismatches
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DOCUMENT-IDENTIFIER: US 5939284 A

TITLE: Protein phosphatase 1 binding protein, R5

DATE-ISSUED: August 17, 1999

INVENTOR-INFORMATION:

NAME CITY STATE ZIP CODE COUNTRY

Cohen; Patricia T. W. Dundee GB
Cohen; Phillip Dundee GB

Young; Peter R. Lawrenceville NJ

US-CL-CURRENT: $\underline{435}/\underline{69.1}$; $\underline{435}/\underline{252.3}$, $\underline{435}/\underline{320.1}$, $\underline{435}/\underline{325}$, $\underline{435}/\underline{455}$, $\underline{536}/\underline{23.1}$, $\underline{536}/\underline{24.31}$

ABSTRACT:

Human PPP1R5 polypeptides and DNA (RNA) encoding such PPP1R5 and a procedure for producing such polypeptides by recombinant techniques is disclosed. Also disclosed are methods for utilizing such PPP1R5, or compounds which inhibit or stimulate PPP1R5 for dysfunctions or diseases which involve resistance to the action of insulin on glycogen synthesis are also disclosed. Agonist and antagonists of these PPP1R5 proteins and methods of their use are also disclosed. Also disclosed are diagnostic assays for detecting diseases related to mutations in the nucleic acid sequences and altered concentrations of the polypeptides. Also disclosed are diagnostic assays for detecting mutations in the polynucleotides encoding the PPP1R5 and for detecting altered levels of the polypeptide in a host.

21 Claims, 5 Drawing figures Exemplary Claim Number: 1 Number of Drawing Sheets: 5

Full Title Citation Front Review Classification Date Reference Sequences Attachments

KWIC Draw, Desc Image

36. Document ID: US 5891430 A

L7: Entry 36 of 46

File: USPT

Apr 6, 1999

US-PAT-NO: 5891430

DOCUMENT-IDENTIFIER: US 5891430 A

TITLE: Diabetogene rad: a type II diabetes specific gene

DATE-ISSUED: April 6, 1999

INVENTOR-INFORMATION:

NAME CITY STATE ZIP CODE COUNTRY

Kahn; C. Ronald West Newton MA Reynet; Christine Boston MA

US-CL-CURRENT: 424/94.6; 435/196, 530/324

ABSTRACT:

Purified DNA including a sequence encoding Diabetogene rad.

5 Claims, 5 Drawing figures Exemplary Claim Number: 2 Number of Drawing Sheets: 5

Full Title Citation Front Review Classification Date Reference Sequences Attachments

KWMC | Drawl Desc | Image

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37. Document ID: US 5859333 A

L7: Entry 37 of 46 File: USPT Jan 12, 1999

US-PAT-NO: 5859333

DOCUMENT-IDENTIFIER: US 5859333 A

TITLE: Plants and processes for obtaining them

DATE-ISSUED: January 12, 1999

INVENTOR-INFORMATION:

NAME CITY STATE ZIP CODE COUNTRY Keeling; Peter Lewis Ames ΙA Lomako; Joseph Miami FL Gieowar-Singh; Dave Miami FLSingletary; George William Ankeny ΤA Whelan; William Joseph Miami FL

US-CL-CURRENT: 800/317.4; 435/101, 435/69.1, 536/23.5, 536/23.6, 800/284, 800/320, 800/320.1

ABSTRACT:

Plants with an altered starch synthesizing ability are produced by incorporating into the genome of the plant at least one donor gene encoding a starch primer. The starch primer is an enzyme capable of initiating starch synthesis, such as an amylogenin and/or glycogenin. DNA constructs encoding a starch primer are provided, particularly constructs encoding amylogenin from maize.

22 Claims, 9 Drawing figures Exemplary Claim Number: 1,8 Number of Drawing Sheets: 9

Full Title Citation Front Review C	Hassification Date Reference Sequences Attachments	KWMC Draww Desc Imag
***** 00 D . ID IIO 6	R40486 A	
38. Document ID: US 58	3 10 100 11	

US-PAT-NO: 5840486

DOCUMENT-IDENTIFIER: US 5840486 A

TITLE: Mutant DNA encoding protein phosphatase 1 G-subunit

DATE-ISSUED: November 24, 1998

INVENTOR-INFORMATION:

NAME CITY STATE ZIP CODE COUNTRY Pedersen; Oluf Holte DK Bj.o slashed.rb.ae butted.k; Christian Boston MA Hansen; Lars Frederiksberg DK Cohen; Patricia Townsend Dundee GB

US-CL-CURRENT: 435/6; 435/195, 435/252.3, 435/320.1, 435/325, 435/91.2, 530/350, 536/23.1, 536/24.3

ABSTRACT:

The present invention relates to a mutant DNA sequence encoding protein phosphatase 1 G-subunit, wherein a mutation of G to T occurs in the position of codon 905 of the coding sequence, a method of detecting a mutation in the gene encoding protein phosphatase 1 G-subunit, as well as a diagnostic composition and a test kit for use in the method.

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22 Claims, 3 Drawing figures Exemplary Claim Number: 1 Number of Drawing Sheets: 3

39. Document ID: US 5795861 A

L7: Entry 39 of 46

File: USPT

Aug 18, 1998

KWWC Draw, Desc Image

US-PAT-NO: 5795861

DOCUMENT-IDENTIFIER: US 5795861 A

TITLE: Methods for regulating gastrointestinal motility

DATE-ISSUED: August 18, 1998

INVENTOR-INFORMATION:

NAME

CITY

Full Title Citation Front Review Classification Date Reference Sequences Attachments

STATE

ZIP CODE

COUNTRY

Kolterman; Orville G.

Rink; Timothy J.

Poway

CA

La Jolla CA

US-CL-CURRENT: 514/12; 514/11, 514/13, 514/866, 530/307, 530/327

ABSTRACT:

Methods for treating conditions associated with elevated, inappropriate or undesired post-prandial blood glucose levels are disclosed which comprise administration of an effective amount of an amylin agonist alone or in conjunction with other anti-gastric emptying agents. Methods for reducing gastric motility and delaying gastric emptying for therapeutic and diagnostic purposes are also described.

6 Claims, 26 Drawing figures Exemplary Claim Number: 1 Number of Drawing Sheets: 12

Full Title Citation Front Review Classification Date Reference Sequences Attachments

KWIC Draw. Desc Image

40. Document ID: US 5684144 A

L7: Entry 40 of 46

File: USPT

Nov 4, 1997

US-PAT-NO: 5684144

DOCUMENT-IDENTIFIER: US 5684144 A

TITLE: Escherichia coli csrA gene, protein encoded thereby, and methods of use thereof

DATE-ISSUED: November 4, 1997

 ${\tt INVENTOR-INFORMATION:}$

NAME CITY

STATE

ZIP CODE

COUNTRY

Romeo; Tony

Arlington

ΤX

US-CL-CURRENT: 536/23.7; 435/252.3, 435/252.33, 435/320.1, 435/69.2, 435/849, 536/23.1

ABSTRACT:

The invention includes a gene encoding csrA, the protein encoded thereby and methods of use thereof.

3 Claims, 24 Drawing figures

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Exemplary Claim Number: 1 Number of Drawing Sheets: 22

Full Title Cit	tation Front	Review Class		Date Re	eference	Sequences	Attachments	KWIC	Draw. Desc
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Search Results - Record(s) 41 through 46 of 46 returned.

41. Document ID: US 5608149 A

L7: Entry 41 of 46

File: USPT

Mar 4, 1997

US-PAT-NO: 5608149

DOCUMENT-IDENTIFIER: US 5608149 A

TITLE: Enhanced starch biosynthesis in tomatoes

DATE-ISSUED: March 4, 1997

INVENTOR-INFORMATION:

NAME CITY

St. Louis

STATE ZIP CODE

COUNTRY

Barry; Gerard F. Kishore; Ganesh M.

Chesterfield

MO MO

Stark; David M.

Fenton

МО

 $\begin{array}{l} \text{US-CL-CURRENT: } \underline{800}/\underline{284}; \ \underline{435}/\underline{101}, \ \underline{435}/\underline{194}, \ \underline{435}/\underline{411}, \ \underline{435}/\underline{69.1}, \ \underline{435}/\underline{69.7}, \ \underline{435}/\underline{69.8}, \ \underline{435}/\underline{70.1}, \\ \underline{536}/\underline{23.2}, \ \underline{536}/\underline{23.4}, \ \underline{536}/\underline{23.7}, \ \underline{536}/\underline{24.1}, \ \underline{800}/\underline{287}, \ \underline{800}/\underline{288}, \ \underline{800}/\underline{317.4} \end{array}$

ABSTRACT:

Promoters for enhanced expression of ADPglucose pyrophosphorylase in potato tubers and fruits such as tomato; methods of using them; DNA molecules, plant cells and plants containing them. A method of decreasing the oil content of seeds by expression of ADPglucose pyrophosphorylase.

16 Claims, 26 Drawing figures Exemplary Claim Number: 9,13 Number of Drawing Sheets: 22

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments

KWC | Drawl Desc | Image

42. Document ID: US 5589374 A

L7: Entry 42 of 46

File: USPT

Dec 31, 1996

US-PAT-NO: 5589374

DOCUMENT-IDENTIFIER: US 5589374 A

TITLE: Diabetogene rad: a type II diabetes specific gene

DATE-ISSUED: December 31, 1996

INVENTOR-INFORMATION:

NAME CITY

STATE

ZIP CODE

COUNTRY

Kahn; C. Ronald

West Newton

MA

Reynet; Christine

Boston

MA

US-CL-CURRENT: 435/69.1; 435/252.3, 435/320.1, 536/23.2, 536/23.5

ABSTRACT:

Purified DNA including a sequence encoding Diabetogene rad.

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8 Claims, 4 Drawing figures Exemplary Claim Number: 2 Number of Drawing Sheets: 4

Full Title Citation Front Review Classification Date Reference Sequences Attachments

KWC Draw Desc Image

43. Document ID: US 5580747 A

L7: Entry 43 of 46

File: USPT

Dec 3, 1996

US-PAT-NO: 5580747

DOCUMENT-IDENTIFIER: US 5580747 A

TITLE: Non-radioactive enzyme assay

DATE-ISSUED: December 3, 1996

INVENTOR - INFORMATION:

NAME

CITY

STATE

ZIP CODE

COUNTRY

Shultz; John W.

Verona

WΙ

White; Douglas H.

Madison

US-CL-CURRENT: $\underline{435/24}$; $\underline{435/15}$, $\underline{435/16}$, $\underline{435/17}$, $\underline{435/18}$, $\underline{435/21}$, $\underline{435/23}$, $\underline{435/4}$, $\underline{435/810}$, $\underline{435/975}$, 436/12, 436/13, 436/14, 436/15, 436/16, 436/17, 436/172, 436/2, 436/63, 436/74, 436/800, 530/300

ABSTRACT:

The present invention is directed to the assay and purification of proteins, and particularly to the non-radioactive assay and purification of protein kinases, phosphatases and protease by incubating the enzyme with a substrate modified peptide to form a product modified peptide under conditions where the enzyme is active. The product modified peptide and substrate modified peptide are then separated, and the product modified peptide is measured. The present invention is also directed to kits and bioreagents for performing the assays.

26 Claims, 20 Drawing figures Exemplary Claim Number: 1 Number of Drawing Sheets: 10

Full Title Citation Front Review Classification Date Reference Sequences Attachments

KWIC Draw Desc Image

44. Document ID: US 5498830 A

L7: Entry 44 of 46

File: USPT

Mar 12, 1996

US-PAT-NO: 5498830

DOCUMENT-IDENTIFIER: US 5498830 A

TITLE: Decreased oil content in plant seeds

DATE-ISSUED: March 12, 1996

INVENTOR - INFORMATION:

NAME CITY

ZIP CODE STATE

COUNTRY

Barry; Gerard F.

St. Louis

MO

Kishore; Ganesh M.

MO

Chesterfield

MO

Stark; David M.

Fenton

US-CL-CURRENT: 800/281; 435/134, 435/194, 536/23.2, 536/23.6, 536/23.7

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ABSTRACT:

Promoters for enhanced expression of ADPglucose pyrophosphorylase in potato tubers and fruits such as tomato; methods of using them; DNA molecules, plant cells and plants containing them. A method of decreasing the oil content of seeds by expression of ADPglucose pyrophosphorylase.

5 Claims, 22 Drawing figures Exemplary Claim Number: 1 Number of Drawing Sheets: 22

Full Title Citation Front Review Classification Date Reference Sequences Attachments

KWMC | Draw, Desc | Image

45. Document ID: US 4472498 A

L7: Entry 45 of 46

File: USPT

Sep 18, 1984

US-PAT-NO: 4472498

DOCUMENT-IDENTIFIER: US 4472498 A

TITLE: Analysis film and a method of analysis using the same

DATE-ISSUED: September 18, 1984

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Masuda; Nobuhito	Kanagawa			JP
Yasuda; Yukio	Kanagawa			JP
Nagatomo; Shigeru	Kanagawa			JP
Makiuchi; Hajime	Kanagawa			JP
Okazaki; Masaki	Kanagawa			JP

ABSTRACT:

An analysis film comprises a reagent layer composed of a porous material which contains an antibody but does not substantially contain a complex of an analyte or a labelled antigen with the antibody. In the analysis film, reagents for enzyme immune reaction of homogenous type are incorporated so that an analyte is analyzed without requiring B/F separation. An analysis method for various analytes using the same provides high sensitivity, high accuracy as well as good reproducibility and is simple and rapid.

19 Claims, 6 Drawing figures Exemplary Claim Number: 1 Number of Drawing Sheets: 1

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments

KWMC | Drawl Desc | Image

46. Document ID: US 4446064 A

L7: Entry 46 of 46

File: USPT

May 1, 1984

US-PAT-NO: 4446064

DOCUMENT-IDENTIFIER: US 4446064 A

TITLE: Insulin mediator substance

DATE-ISSUED: May 1, 1984

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* *	

INVENTOR-INFORMATION:

NAME

Record List Display

CITY

STATE

ZIP CODE

COUNTRY

Larner; Joseph

Charlottesville Charlottesville VA

Cheng; Kang Galasko; Gail

Johannesburg

VA

 z_{A}

US-CL-CURRENT: 530/344; 424/548, 530/305, 530/841

ABSTRACT:

An insulin mediator substance produced by the process comprising: contacting muscle tissue with insulin; deproteinizing the muscle tissue; removing the major nucleotides from the deproteinized muscle tissue; chromatographing the so-treated product on a Sephadex G-25 column using 0.05 N formic acid; and recovering the fraction wherein the major 230-nm absorbance peak corresponds with the ninhydrin-positive peak.

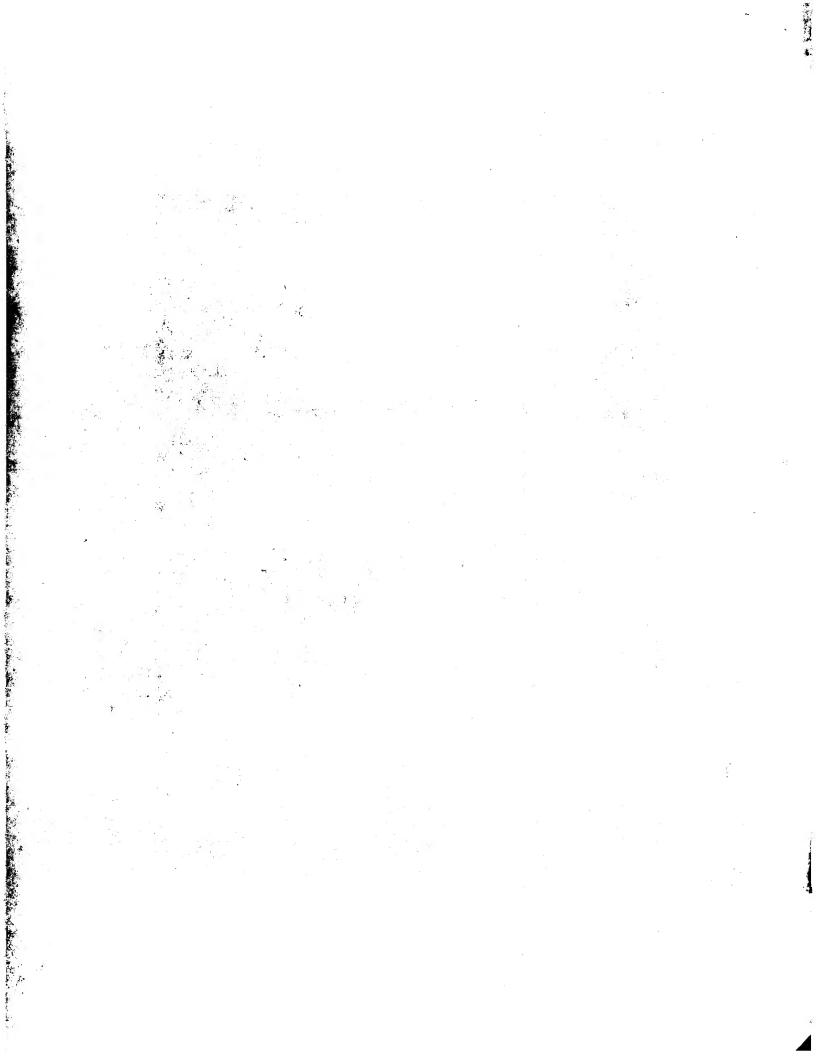
10 Claims, 2 Drawing figures Exemplary Claim Number: 1 Number of Drawing Sheets: 1

Full Title Citation Fro	nt Review	Classification	Date Refe	rence Sequences	Attachments	KWMC Drawn Desc
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(from 402 .+-. 54 to 173 .+-. 27 .mu.g of glycogen/mg of protein) in the fasted vs. fed states compared with only 44% in GL-overexpressing animals (from 740 .+-. 35 to 413 .+-. 141 .mu.g of glycogen/mg of protein). Since the OGTT studies were performed on 20-h fasted rats, this meant that

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GM. DELTA. C-overexpressing rats synthesized much more glycogen than GL-overexpressing HF rats during the OGTT (419 vs. 117 .mu.g of glycogen/mg of protein, resp.), helping to explain why GM.DELTA.C preferentially enhanced glucose clearance. We conclude that GM.DELTA.C has a unique combination of glycogenic potency and responsiveness to glycogenolytic signals that allows it to be used to lower blood glucose levels in diabetes.

REFERENCE COUNT:

THERE ARE 33 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L29 ANSWER 2 OF 6 CAPLUS COPYRIGHT 2003 ACS

ACCESSION NUMBER: DOCUMENT NUMBER:

2002:79805 CAPLUS

136:260338

TITLE:

Glycogen-targeting subunits and glucokinase

differentially affect pathways of glycogen metabolism

and their regulation in hepatocytes

AUTHOR(S):

Yang, Ruojing; Cao, Liwei; Gasa, Rosa; Brady, Matthew

J.; Sherry, A. Dean; Newgard, Christopher B.

CORPORATE SOURCE:

Departments of Biochemistry and Internal Medicine, the Touchstone Center for Diabetes Research, University of Texas Southwestern Medical Center, Dallas, TX, 75390,

HSA

SOURCE:

Journal of Biological Chemistry (2002), 277(2),

1514-1523

CODEN: JBCHA3; ISSN: 0021-9258

PUBLISHER:

American Society for Biochemistry and Molecular

Biology

DOCUMENT TYPE:

Journal

LANGUAGE: English Overexpression of the glucose-phosphorylating enzyme glucokinase (GK) or

members of the family of glycogen-targeting subunits of protein phosphatase-1 increases hepatic glucose disposal and glycogen synthesis. This study was undertaken to evaluate the functional properties of a novel, truncated glycogen-targeting subunit derived from the skeletal muscle isoform GM/RG1 and to compare pathways of glycogen metab. and their regulation in cells with overexpressed targeting subunits and GK. When overexpressed in hepatocytes, truncated GM/RG1 (GM.DELTA.C) was approx. twice as potent as full-length GM/RGl in stimulation of glycogen synthesis, but clearly less potent than GK or two other native glycogen-targeting subunits, GL and PTG. We also found that cells with overexpressed GM.DELTA.C are unique in that glycogen was efficiently degraded in response to lowering of media glucose concns., stimulation with forskolin, or a combination of both maneuvers, whereas cells with overexpressed GL, PTG, or GK exhibited impairment in one or both of these glycogenolytic signaling pathways. 2H NMR anal. of purified glycogen revealed that hepatocytes with overexpressed GK synthesized a larger portion of their glycogen from triose phosphates and a smaller portion from tricarboxylic acid cycle intermediates than cells with overexpressed glycogen-targeting subunits. Addnl. evidence for activation of distinct pathways of glycogen synthesis by GK and targeting subunits is provided by the additive effect of co-overexpression of the two types of proteins upon glycogen synthesis and a much larger stimulation of glucose utilization, glucose transport, and lactate prodn. elicited by GK. We conclude that overexpression of the novel targeting subunit GM.DELTA.C confers unique regulation of glycogen metab. Furthermore, targeting subunits and GK stimulate glycogen synthesis by distinct pathways.

REFERENCE COUNT:

THERE ARE 36 CITED REFERENCES AVAILABLE FOR THIS 36 RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L29 ANSWER 3 OF 6 SCISEARCH COPYRIGHT 2003 ISI (R)

ACCESSION NUMBER:

97:636960 SCISEARCH

THE GENUINE ARTICLE: XG123

TITLE:

Analysis of type-1 protein phosphatase

glycogen-targeting subunit

mRNA in skeletal muscle of Pima Indians Xia X (Reprint); Bogardus C; Prochazka M

CORPORATE SOURCE:

NIDDK, CDNS, NIH, PHOENIX, AZ

COUNTRY OF AUTHOR:

USA

SOURCE:

AUTHOR:

DIABETOLOGIA, (JUN 1997) Vol. 40, Supp. [1], pp. 621-621. Publisher: SPRINGER VERLAG, 175 FIFTH AVE, NEW YORK, NY

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ISSN: 0012-186X.

DOCUMENT TYPE: Conference; Journal

LIFE; CLIN FILE SEGMENT: LANGUAGE: English

REFERENCE COUNT:

L29 ANSWER 4 OF 6 SCISEARCH COPYRIGHT 2003 ISI (R) ACCESSION NUMBER: 97:413159 SCISEARCH

THE GENUINE ARTICLE: WX380

TITLE: Analysis of type-1 protein phosphatase

glycogen-targeting subunit

mRNA in skeletal muscle of nondiabetic Pima Indians.

Xia X L (Reprint); Bogardus C; Prochazka M AUTHOR:

SOURCE: DIABETES, (MAY 1997) Vol. 46, Supp. [1], pp. 302-302.

Publisher: AMER DIABETES ASSOC, 1660 DUKE ST, ALEXANDRIA,

VA 22314.

ISSN: 0012-1797. Conference; Journal

DOCUMENT TYPE: LIFE; CLIN FILE SEGMENT:

LANGUAGE: English

REFERENCE COUNT:

L29 ANSWER 5 OF 6 CAPLUS COPYRIGHT 2003 ACS ACCESSION NUMBER: 1997:747992 CAPLUS

DOCUMENT NUMBER: 128:151047

PPP1R6, a novel member of the family of TITLE:

glycogen-targetting subunits of protein phosphatase 1 AUTHOR (S): Armstrong, Christopher G.; Browne, Gareth J.; Cohen,

Philip; Cohen, Patricia T. W.

Department of Biochemistry, Medical Research Council CORPORATE SOURCE:

Protein Phosphorylation Unit, University of Dundee,

Dundee, DD1 4HN, UK

SOURCE: FEBS Letters (1997), 418(1,2), 210-214

CODEN: FEBLAL; ISSN: 0014-5793

PUBLISHER: Elsevier Science B.V.

DOCUMENT TYPE: Journal LANGUAGE: English

A complementary DNA encoding a novel human protein phosphatase 1 (PP1) glycogen-targeting subunit of mol. mass 33 kDa has been sequenced. PPP1R6 is 31% identical to the glycogen-targeting subunit (GL) of PP1 from rat liver, 28% identical to the N-terminal region of the glycogen-targeting subunit (GM) from human skeletal muscle and 27% identical to glycogen-targeting subunit PPP1R5. Unlike human PPP1R5 and its murine homolog PTG, whose mRNAs are most abundant in skeletal muscle, heart and liver, PPP1R6 is present at similar levels in a wide variety of tissues. The PPP1R6 is assocd. with glycogen in muscle but is not subject to the same modes of covalent and allosteric regulation as GM and GL.

L29 ANSWER 6 OF 6 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.

ACCESSION NUMBER: 1997:370905 BIOSIS

DOCUMENT NUMBER:

PREV199799670108

TITLE:

Analysis of type-1 protein phosphatase

glycogen-targeting subunit mRNA in skeletal muscle of Pima Indians. Xia, X.; Bogardus, C.; Prochazka, M.

CORPORATE SOURCE:

CDNS-NIDDK-NIH, Phoenix, AZ USA

AUTHOR(S): SOURCE:

Diabetologia, (1997) Vol. 40, No. SUPPL. 1, pp. A159. Meeting Info.: 16th International Diabetes Federation

Congress Helsinki, Finland July 20-25, 1997

ISSN: 0012-186X.

DOCUMENT TYPE:

Conference; Abstract; Conference

LANGUAGE:

English

=> s 17 and 121TOTAL FOR ALL FILES 0 L7 AND L21

=> s 17 and glycogen targeting TOTAL FOR ALL FILES

L43 17 L7 AND GLYCOGEN TARGETING

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=> dup rem 143

PROCESSING COMPLETED FOR L43

6 DUP REM L43 (11 DUPLICATES REMOVED)

=> d ibib abs

L44 ANSWER 1 OF 6

MEDLINE

DUPLICATE 1

ACCESSION NUMBER: DOCUMENT NUMBER:

2002138625

MEDLINE

TITLE:

21861581 PubMed ID: 11872655

Human skeletal muscle expresses a glycogentargeting subunit of PP1 that is identical to the

insulin-sensitive glycogen-targeting

subunit G(L) of liver.

AUTHOR:

Munro Shonagh; Cuthbertson Daniel J R; Cunningham Joan;

Sales Mark; Cohen Patricia T W

CORPORATE SOURCE:

Medical Research Council Protein Phosphorylation Unit,

School of Life Sciences, University of Dundee, Dundee,

Scotland, U.K.

SOURCE:

DIABETES, (2002 Mar) 51 (3) 591-8. Journal code: 0372763. ISSN: 0012-1797.

PUB. COUNTRY:

United States

DOCUMENT TYPE:

Journal; Article; (JOURNAL ARTICLE)

LANGUAGE:

English

FILE SEGMENT:

Abridged Index Medicus Journals; Priority Journals

ENTRY MONTH: 200203

ENTRY DATE:

Entered STN: 20020305

Last Updated on STN: 20020317 Entered Medline: 20020315

AB Insulin has been previously shown to regulate the expression of the hepatic glycogen-targeting subunit, G(L), of protein

phosphatase 1 (PP1) and is believed to control the activity of the PP1-G(L) complex by modulation of the level of phosphorylase a, which allosterically inhibits the activity of PP1-G(L). These mechanisms contribute to the ability of insulin to increase hepatic glycogen synthesis. Human G(L) shows >88% amino acid identity to its rat and mouse homologs, with complete conservation of the phosphorylase a binding site. G(L) is highly expressed

in the liver and present at appreciable levels in heart tissue of all three species. Surprisingly, G(L) is highly expressed in human skeletal muscle while only being detected at very low levels in rat, mouse, and rabbit skeletal muscle. The amino acid sequence of G(L) predicted from the cDNA is identical in human liver and skeletal muscle and encoded by a gene on chromosome 8 at p23.1. The species-specific difference in the level of expression of G(L) mRNA and protein in skeletal muscle has important implications for understanding the mechanisms by which insulin regulates glycogen synthesis in human skeletal muscle and for questions regarding whether rodents are appropriate models for this purpose.

=> d ibib abs 2-6

L44 ANSWER 2 OF 6 MEDLINE

ACCESSION NUMBER: DOCUMENT NUMBER:

2002485047

MEDLINE

22234049 PubMed ID: 12297011

TITLE: Epinephrine control of glycogen metabolism in

glycogen-associated protein phosphatase PP1G/R(GL) knockout

mice.

AUTHOR:

Kim Jong Hwa; DePaoli-Roach Anna A

CORPORATE SOURCE:

Division of Food Science and Nutrition, Woosuk University, Jeonbuk, 565-701, Republic of Korea.. jhkim@woosuk.ac.kr

SOURCE:

J Biochem Mol Biol, (2002 May 31) 35 (3) 283-90. Journal code: 9702084. ISSN: 1225-8687.

PUB. COUNTRY:

DOCUMENT TYPE:

Korea (South) Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: Enalish

FILE SEGMENT:

Priority Journals 200212

ENTRY MONTH: ENTRY DATE:

Entered STN: 20020926

Last Updated on STN: 20021217 Entered Medline: 20021203

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The glycogen-associated protein phosphatase (PP1G/ R(GL)) may play a central role in the hormonal control of glycogen metabolism in the skeletal muscle. Here, we investigated the in vivo epinephrine effect of glycogen metabolism in the skeletal muscle of the wild-type and R(GL) knockout mice. The administration of epinephrine increased blood glucose levels from 200 +/- +/- 20 to 325 +/- 20 mg/dl in both wild-type and knockout mice. Epinephrine decreased the glycogen synthase -/+ G6P ratio from 0.24 +/- 0.04 to 0.10 +/- 0.02 in the wild-type, and from 0.17 +/-0.02 to 0.06 \pm 0.01 in the knockout mice. Conversely, the glycogen phosphorylase activity ratio increased from 0.21 +/- 0.04 to 0.65 +/- 0.07 and from 0.30 +/- 0.04 to 0.81 +/- 0.06 in the epinephrine treated wild-type and knockout mice respectively. The glycogen content of the knockout mice was substantially lower (27 percent) than that of both wild-type mice; and epinephrine decreased glycogen content in the wild-type and knockout mice. Also, in Western blot analysis there was no compensation of the other glycogen targeting components PTG/R5 and R6 in the knockout mice compared with the wild-type. Therefore, R(GL) is not required for the epinephrine stimulation of glycogen metabolism, and rather another phosphatase and/or regulatory subunit appears to be involved.

L44 ANSWER 3 OF 6 CAPLUS COPYRIGHT 2003 ACS ACCESSION NUMBER: 2000:161323 CAPLUS

DOCUMENT NUMBER:

132:204861

TITLE:

Protein domains in the hepatic glycogentargeting subunit of protein phosphatase 1 and their use in modulation of blood glucose levels

INVENTOR(S):

Cohen, Patricia Townsend Wade; Armstrong, Christopher

George; Doherty, Martin John Medical Research Council, UK

PATENT ASSIGNEE(S):

PCT Int. Appl., 51 pp.

SOURCE:

CODEN: PIXXD2

DOCUMENT TYPE:

Patent

LANGUAGE:

English

FAMILY ACC. NUM. COUNT:

PATENT INFORMATION:

APPLICATION NO. DATE PATENT NO. KIND DATE ______ -----WO 2000012549 A1 20000309 WO 1999-GB2761 19990819 W: AU, CA, JP, US RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE CA 1999-2340885 19990819 CA 2340885 AA 20000309 AU 9954368 A1 20000321 AU 1999-54368 19990819 EP 1107986 A1 20010620 EP 1999-940382 19990819 R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE. FI JP 2002532381 T2 20021002 JP 2000-567566 19990819 A 19980827 W 19990819 GB 1998-18650 PRIORITY APPLN. INFO.: WO 1999-GB2761

Three functional domains are identified in the glycogentargeting subunit (GL) of rat liver protein phosphatase 1. Amino acid residues 94-267 of GL are required for binding to glycogen, the phosphorylase a-binding site lies in the C-terminal 16 amino acids, and the protein phosphatase 1-binding domain lies between residues 59 and 94. The present invention relates to to the C-terminal 16-amino acid domain (PEWPSYGYEKLYPYY) domain, which is useful for treating disorders assocd. with abnormal blood glucose levels in mammals, such as Type I and Type II diabetes. The invention also relates to methods of making and using the peptide and related compds. which block the interaction of phosphorylase a with GL of protein phosphatase 1.

REFERENCE COUNT:

THERE ARE 5 CITED REFERENCES AVAILABLE FOR THIS 5 RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L44 ANSWER 4 OF 6 CAPLUS COPYRIGHT 2003 ACS ACCESSION NUMBER: 2000:627758 CAPLUS

DOCUMENT NUMBER:

133:279255

TITLE:

Distinctive regulatory and metabolic properties of

glycogen-targeting subunits of

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The state of the s

protein phosphatase-1 (PTG, GL, GM/RG1) expressed in

hepatocytes

AUTHOR(S): Gasa, Rosa; Jensen, Per B.; Berman, Hal K.; Brady,

Matthew J.; DePaoli-Roach, Anna A.; Newgard,

Christopher B.

CORPORATE SOURCE: Department of Biochemistry & Internal Medicine and

Touchstone Center for Diabetes Research, University of Texas Southwestern Medical Center, Dallas, TX, 75235,

USA

SOURCE: Journal of Biological Chemistry (2000), 275(34),

26396-26403

CODEN: JBCHA3; ISSN: 0021-9258

PUBLISHER: American Society for Biochemistry and Molecular

Biology Journal

DOCUMENT TYPE: Journal LANGUAGE: English

AB Glycogen-targeting subunits of protein phosphatase-1

facilitate interaction of the phosphatase with enzymes of glycogen metab. We have shown that overexpression of one member of the family, protein targeting to glycogen (PTG), causes large increases in glycogen storage in isolated hepatocytes or intact rat liver. In the current study, we have compared the metabolic and regulatory properties of PTG (expressed in many tissues), with two other members of the gene family, GL (expressed primarily in liver) and GM/RGl (expressed primarily in striated muscle). Adenovirus-mediated expression of these proteins in hepatocytes led to the following key observations. GL has the highest glycogenic potency among the three forms studied. Glycogen synthase activity ratio is much higher in GL-overexpressing cells than in PTG or GM/RG1-overexpressing cells. Thus, at moderate levels of GL overexpression, glycogen synthase activity is increased by insulin treatment, but at higher levels of GL expression, insulin is no longer required to achieve maximal synthase activity. In contrast, cells with high levels of PTG overexpression retain dose-dependent regulation of glycogen synthesis and glycogen synthase enzyme activity by insulin. GL- and GM/RGl-overexpressing cells exhibit a strong glycogenolytic response to forskolin, whereas PTG-overexpressing cells are less responsive. This difference may be explained in part by a lesser forskolin-induced increase in glycogen phosphorylase activity in PTG-overexpressing cells. Based on these results, we suggest that expression of either GL or GM/RGl in liver of diabetic animals may

represent a strategy for lowering of blood glucose levels in diabetes.

REFERENCE COUNT: 26 THERE ARE 26 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L44 ANSWER 5 OF 6 MEDLINE DUPLICATE 2

ACCESSION NUMBER: 1999059701 MEDLINE

DOCUMENT NUMBER: 99059701 PubMed ID: 9841883

TITLE: Identification of the separate domains in the hepatic

glycogen-targeting subunit of protein
phosphatase 1 that interact with phosphorylase

a, glycogen and protein phosphatase 1.

AUTHOR: Armstrong C G; Doherty M J; Cohen P T

CORPORATE SOURCE: Medical Research Council Protein Phosphorylation Unit,

Department of Biochemistry, University of Dundee, Dundee DD15EH, Scotland, U.K.. cgarmstrong@bad.dundee.ac.uk

SOURCE: BIOCHEMICAL JOURNAL, (1998 Dec 15) 336 (Pt 3) 699-704.

Journal code: 2984726R. ISSN: 0264-6021.

PUB. COUNTRY: ENGLAND: United Kingdom

DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

ENTRY MONTH: 199902

ENTRY DATE: Entered STN: 19990311

Last Updated on STN: 19990311 Entered Medline: 19990225

Deletion and mutational analyses of the rat liver glycogentargeting subunit (GL) of protein phosphatase 1 (PP1) have identified three separate domains that are responsible for binding of PP1, glycogen and phosphorylase a. The glycogen-binding domain spans the centre of GL between residues 144 and 231 and appears to be distinct from the glycogen-binding (storage) site of phosphorylase. The regulatory high-affinity binding site for phosphorylase

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a lies in the 16 amino acids at the C-terminus of GL. The PP1-binding domain is deduced to comprise the -RVXF- motif [Egloff, Johnson, Moorhead, Cohen and Barford (1997) EMBO J. 16, 1876-1887] located at residues 61-64 of GL and preceding lysine residues at positions 56, 57 and 59. A possible approach for increasing glycogen synthesis in certain disorders is discussed.

DUPLICATE 3 L44 ANSWER 6 OF 6 MEDLINE

ACCESSION NUMBER: 97390464 MEDLINE

DOCUMENT NUMBER: 97390464 PubMed ID: 9242697

TITLE: Role of protein targeting to glycogen (PTG) in the

regulation of protein phosphatase-1 activity.

Brady M J; Printen J A; Mastick C C; Saltiel A R AUTHOR .

CORPORATE SOURCE: Department of Cell Biology, Parke-Davis Pharmaceutical Research Division, Warner-Lambert Company, Ann Arbor,

Michigan 48105, USA.

SOURCE: JOURNAL OF BIOLOGICAL CHEMISTRY, (1997 Aug 8) 272 (32)

20198-204.

Journal code: 2985121R. ISSN: 0021-9258.

United States PUB. COUNTRY:

Journal; Article; (JOURNAL ARTICLE)

DOCUMENT TYPE:

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LANGUAGE: English

FILE SEGMENT: Priority Journals 199709 ENTRY MONTH:

ENTRY DATE: Entered STN: 19970922

Last Updated on STN: 19970922 Entered Medline: 19970905

AB We have recently cloned from 3T3-L1 adipocytes a novel glycogentargeting subunit of protein phosphatase-1, termed PTG (Printen, J. A., Brady, M. J., and Saltiel, A. R. (1997) Science 275, 1475-1478). Differentiation of 3T3-L1 fibroblasts into highly insulin-responsive adipocytes resulted in a marked increase in PTG expression. Immobilized glutathione S-transferase (GST)-PTG fusion protein specifically bound either PP1 or phosphorylase a. Addition of soluble GST-PTG to 3T3-L1 lysates increased PP1 activity against 32P-labeled phosphorylase a by decreasing the Km of PP1 for phosphorylase 5-fold, while having no effect on the Vmax of the dephosphorylation reaction. Alternatively, PTG did not affect PP1 activity against hormone-sensitive lipase. PTG was not a direct target of intracellular signaling, as insulin or forskolin treatment of cells did not activate a kinase capable of phosphorylating PTG in vivo or in vitro. Finally, PTG decreased the ability of DARPP-32 to inhibit PP1 activity from 3T3-L1 adipocyte lysates. These data cumulatively suggest that PTG increases PP1 activity against specific proteins by several distinct

=> s 17 and protein phosphatase

TOTAL FOR ALL FILES

mechanisms.

960 L7 AND PROTEIN PHOSPHATASE

=> s 151 and (inhibitor or agonist or antagonist or bind?)

TOTAL FOR ALL FILES

L58 642 L51 AND (INHIBITOR OR AGONIST OR ANTAGONIST OR BIND?)

=> s 158 and diabetes

TOTAL FOR ALL FILES

L65 7 L58 AND DIABETES

=> dup rem 165

PROCESSING COMPLETED FOR L65

4 DUP REM L65 (3 DUPLICATES REMOVED)

=> d ibib abs 1-4

L66 ANSWER 1 OF 4 SCISEARCH COPYRIGHT 2003 ISI (R)

ACCESSION NUMBER: 2002:1212 SCISEARCH

THE GENUINE ARTICLE: 502GZ

TITLE: The level of the glycogen targetting regulatory subunit R5

of protein phosphatase 1 is decreased

in the livers of insulin-dependent diabetic rats and

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Browne G J; Delibegovic M; Keppens S; Stalmans W; Cohen P AUTHOR:

T W (Reprint)

CORPORATE SOURCE: Univ Dundee, Sch Life Sci, MRC, Prot Phosphorylat Unit,

MSI WTB Complex, Dow St, Dundee DD1 5EH, Scotland (Reprint); Univ Dundee, Sch Life Sci, MRC, Prot

Phosphorylat Unit, Dundee DD1 5EH, Scotland; Katholieke Univ Leuven, Fac Geneeskunde, Afeling Biochem, B-3000

Louvain, Belgium

COUNTRY OF AUTHOR:

Scotland; Belgium

SOURCE:

BIOCHEMICAL JOURNAL, (1 DEC 2001) Vol. 360, Part 2, pp.

Publisher: PORTLAND PRESS, 59 PORTLAND PLACE, LONDON WIN

3AJ, ENGLAND. ISSN: 0264-6021. Article; Journal

DOCUMENT TYPE: LANGUAGE:

English

REFERENCE COUNT:

45

ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

Hepatic glycogen synthesis is impaired in insulin-dependent diabetic AB rats owing to defective activation of glycogen synthase by glycogen-bound protein phosphatase I (PPI). The identification of three glycogen-targetting subunits in liver, G(L)R5/PTG and R6, which form complexes with the catalytic subunit of PP1 (PP1c), raises the question of whether some or all of these PP1c complexes are subject to regulation by insulin. In liver lysates of control rats, R5 and R6 complexes with PPlc were found to contribute significantly (16 and 21%. respectively) to the phosphorylase phosphatase activity associated with the glycogen-targetting subunits, G(L)-PP1c accounting for the remainder (63%). In liver lysates of insulin-dependent diabetic and of starved rats, the phosphorylase phosphatase activities of the R5 and G(L) complexes with PP1c were shown by specific immunoadsorption assays to be substantially decreased, and the levels of R5 and G(L) were shown by immunoblotting to be much lower than those in control extracts. The phosphorylase phosphatase activity of R6-PP1c and the concentration of R6 protein were unaffected by these treatments. Insulin administration to diabetic rats restored the levels of R5 and G(L) and their associated activities. The regulation of R5 protein levels by insulin was shown to correspond to changes in the level of the mRNA, as has been found for G(L). The in vitro glycogen synthase phosphatase/phosphorylase phosphatase activity ratio of R5-PPlc was lower than that of G(L)-PPlc, suggesting that R5-PPlc may function as a hepatic phosphorylase phosphatase, whereas G(L)-PPlc may be the major hepatic glycogen synthase phosphatase. In hepatic lysates, more than half the R6 was present in the glycogen-free supernatant, suggesting that R6 may have lower affinity for glycogen than R5 and G(L).

L66 ANSWER 2 OF 4 CAPLUS COPYRIGHT 2003 ACS ACCESSION NUMBER: 2000:161323 CAPLUS

DOCUMENT NUMBER:

132:204861

TITLE:

Protein domains in the hepatic glycogen-targeting

subunit of protein phosphatase 1

and their use in modulation of blood glucose levels Cohen, Patricia Townsend Wade; Armstrong, Christopher

George; Doherty, Martin John Medical Research Council, UK

PCT Int. Appl., 51 pp.

SOURCE:

INVENTOR(S):

CODEN: PIXXD2

DOCUMENT TYPE:

Patent

LANGUAGE:

English

FAMILY ACC. NUM. COUNT:

PATENT INFORMATION:

PATENT ASSIGNEE(S):

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 20000125	49 Al	20000309	WO 1999-GB2761	19990819
W: AU,	CA, JP, US			
RW: AT,	BE, CH, CY	, DE, DK, ES,	FI, FR, GB, GR, IE,	IT, LU, MC, NL,
PT,	SE			
CA 2340885	AA	20000309	CA 1999-2340885	19990819
AU 9954368	A1	20000321	AU 1999-54368	19990819
EP 1107986	A1	20010620	EP 1999-940382	19990819

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R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT,

JP 2002532381 T2 20021002 JP 2000-567566 19990819 A 19980827 GB 1998-18650 PRIORITY APPLN. INFO.: WO 1999-GB2761 W 19990819

Three functional domains are identified in the glycogen-targeting subunit (GL) of rat liver protein phosphatase 1. Amino acid

residues 94-267 of GL are required for binding to glycogen, the

phosphorylase a-binding site lies in the

C-terminal 16 amino acids, and the protein phosphatase 1-binding domain lies between residues 59 and 94. The present invention relates to to the C-terminal 16-amino acid domain (PEWPSYGYEKLYPYY) domain, which is useful for treating disorders assocd. with abnormal blood glucose levels in mammals, such as Type I and Type II diabetes. The invention also relates to methods of making and using the peptide and related compds. which block the interaction of phosphorylase a with GL of protein

phosphatase 1.

5 THERE ARE 5 CITED REFERENCES AVAILABLE FOR THIS REFERENCE COUNT: RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L66 ANSWER 3 OF 4 MEDLINE DUPLICATE 1

ACCESSION NUMBER: 91378572

DOCUMENT NUMBER: PubMed ID: 1654859 91378572

Protein phosphatase-1 and -2A, kinase TITLE:

FA, and casein kinase II in skeletal muscle of

MEDLINE

streptozotocin diabetic rats. AUTHOR: Metallo A; Villa-Moruzzi E

CORPORATE SOURCE: Dipartimento di Biomedicina Sperimentale, Universita di

Pisa, Italy.

SOURCE: ARCHIVES OF BIOCHEMISTRY AND BIOPHYSICS, (1991 Sep) 289 (2)

382-6. Journal code: 0372430. ISSN: 0003-9861.

PUB. COUNTRY: United States

DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

ENTRY MONTH: 199110

Entered STN: 19911108 ENTRY DATE:

Last Updated on STN: 19980206 Entered Medline: 19911024

AB Protein phosphatase-1 (PP-1) and -2A (PP-2A), two regulatory subunits of PP-1, the glycogen-binding subunit ${\tt G}$ and inhibitor-2 (I-2), kinase FA, and casein kinase II (CK-II) were investigated in skeletal muscle of diabetic rats 2 days after streptozotocin injection. FA and CK-II activate PP-1 in vitro and might be involved in the activation of PP-1 by insulin. Following muscle fractionation we found that (1) diabetes decreased both basal and trypsin-stimulated PP-1 activities; the decrease was more significant in the glycogen-bound and microsomal fractions than in the cytosol (cytosolic PP-1 decreased as specific activity but not as activity/g of muscle); also PP-2A was lower in diabetic cytosols; (2) less G was immunoprecipitated from diabetic glycogen-bound fractions compared to controls, while I-2 was not significantly changed; (3) diabetes decreased also FA (assayed as PP-1 activator) and CK-II (assayed using a synthetic peptide as substrate); (4) diabetes did not have any effect on phosphorylase (a + b) activity in the glycogen-bound fraction. Altogether the data show that acute diabetes decreased PP-1, one of its regulatory subunits and two potentially physiological regulators of PP-1, in addition to PP-2A. This may indicate that insulin is responsible for the long-term regulation of the same enzymes that are also under acute insulin control.

L66 ANSWER 4 OF 4 MEDLINE DUPLICATE 2

ACCESSION NUMBER: 85127002 MEDLINE

DOCUMENT NUMBER -85127002 PubMed ID: 2982604

TITLE: Insulin-induced increases in the activity of the spontaneously active and ATP.Mg-dependent forms of

phosphatase-1 in alloxan-diabetic rat liver.

Dragland-Meserve C J; Webster D K; Parker Botelho L H AUTHOR: SOURCE: EUROPEAN JOURNAL OF BIOCHEMISTRY, (1985 Feb 1) 146 (3)

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699-704.

Journal code: 0107600. ISSN: 0014-2956. GERMANY, WEST: Germany, Federal Republic of

PUB. COUNTRY: DOCUMENT TYPE:

Journal; Article; (JOURNAL ARTICLE)

LANGUAGE:

English

FILE SEGMENT:

Priority Journals

ENTRY MONTH:

198503

ENTRY DATE:

Entered STN: 19900320

Last Updated on STN: 19970203

Entered Medline: 19850327

Liver supernatant from normal and alloxan-diabetic rats was fractionated by DEAE-cellulose chromatography and the separated phosphoprotein phosphatase fractions were assayed with [32P]histone f2b, [32P]

phosphorylase a and [32P]phosphorylase kinase as substrates. In diabetic rat liver, one of the phosphatase fractions found in the normal liver was significantly reduced. This fraction was identified as a mixture of the spontaneously active form and the ATP . Mg-dependent form of phosphoprotein phosphatase-1 (Fc) based on sensitivity to inhibitor-2, substrate specificity, and the fact that it could be activated 42-70% by glycogen synthase kinase-3 in the presence of ATP . Mq. Further analysis of this fraction showed that liver cytosol from diabetic rats contained 62-79% lower spontaneously active phosphatase-1 activity and 40-51% lower combined spontaneously active and ATP . Mg-dependent protein phosphatase-1 (Fc)

activity. Insulin administration increased the spontaneously active and the ATP . Mg-dependent protein phosphatase-1

activities approximately 45% and 36%, respectively, in alloxan-diabetic rats. These data imply that the lower levels of spontaneously active phosphatase-1 activity in diabetic rat liver cannot be explained by presuming phosphatase-1 to have been present as Fc, the inactive form. Moreover, insulin restored the total activity of the spontaneously active and activatable forms of phosphatase-1 to those present in normal liver implying that both forms of phosphatase-1 activity are under hormonal control.

=> s 158 and glucose TOTAL FOR ALL FILES

86 L58 AND GLUCOSE

=> dup rem 173

PROCESSING COMPLETED FOR L73

31 DUP REM L73 (55 DUPLICATES REMOVED)

=> s 131 not 2000-2003/py

TOTAL FOR ALL FILES

0 L31 NOT 2000-2003/PY

=> d 174 ibib abs 1-31

DUPLICATE 1 L74 ANSWER 1 OF 31 MEDITNE

ACCESSION NUMBER: 2001407861 MEDLINE

21351803 PubMed ID: 11459182 DOCUMENT NUMBER:

Characterization of Gaclp, a regulatory subunit of ${f protein\ phosphatase}$ type I involved in TITLE:

glycogen accumulation in Saccharomyces cerevisiae.

AUTHOR: Wu X; Hart H; Cheng C; Roach P J; Tatchell K

CORPORATE SOURCE: Department of Biochemistry and Molecular Biology, Louisiana

State University Medical Center, Shreveport 71130, USA.

DK20542 (NIDDK) CONTRACT NUMBER:

DK42576 (NIDDK) GM477899 (NIGMS)

SOURCE: Mol Genet Genomics, (2001 Jun) 265 (4) 622-35.

Journal code: 101093320. ISSN: 1617-4615. Germany: Germany, Federal Republic of

DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE) LANGUAGE: English

FILE SEGMENT: Priority Journals

ENTRY MONTH: 200108

PUB. COUNTRY:

ENTRY DATE: Entered STN: 20010820

Last Updated on STN: 20010820

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Entered Medline: 20010816

 $\mbox{GAC1}$ and $\mbox{GLC7}$ encode regulatory and catalytic subunits, respectively, of a AB type 1 phosphatase (PP1) in Saccharomyces cerevisiae that controls glycogen synthesis by regulating the phosphorylation state of glycogen synthase (Gsy2p). To investigate the role of Gaclp in this process, a set of GAC1 deletions were tested for their ability to complement a gac1 null mutation and to associate with Glc7p and with Gsy2p. The N-terminal 93 amino acids of Gaclp are necessary and sufficient for the interaction with Glc7p, whereas a region spanning residues 130-502 is required for Gsy2p binding. Both domains are required for full activity in vivo, although the Glc7p-binding domain retains some residual activity and can alter the phosphorylase a phosphatase activity of Glc7p in vitro. Further mutational analysis showed that Val71 and Phe73 of Gaclp are necessary for binding to Glc7p, while Asn356 and Tyr357 of Gaclp are necessary for binding to Gsy2p. These results suggest that Gaclp targets PPI to its substrate Gsy2p and that Gacip may alter the catalytic activity of PP . Our data also show that overexpression of Gaclp affects glucose repression and ion homeostasis, two additional targets of GLC7, suggesting that multiple regulatory subunits compete for Glc7p binding in vivo.

MEDLINE L74 ANSWER 2 OF 31 DUPLICATE 2 MEDLINE

2001461224 ACCESSION NUMBER:

DOCUMENT NUMBER: 21397180 PubMed ID: 11506360

Partial purification and biochemical characterization of a TITLE:

heteromeric protein phosphatase 2A

holoenzyme from maize (Zea mays L.) leaves that dephosphorylates C4 phosophoenolpyruvate carboxylase.

Dong L; Ermolova N V; Chollet R AUTHOR:

Department of Biochemistry, University of Nebraska-Lincoln, CORPORATE SOURCE:

George W. Beadle Center, 68588-0664, USA.

PLANTA, (2001 Jul) 213 (3) 379-89. SOURCE:

Journal code: 1250576. ISSN: 0032-0935. Germany: Germany, Federal Republic of Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

PUB. COUNTRY: DOCUMENT TYPE:

FILE SEGMENT: Priority Journals

ENTRY MONTH: 200206

ENTRY DATE: Entered STN: 20010820

> Last Updated on STN: 20020625 Entered Medline: 20020624

The activity and allosteric properties of plant phosphoenolpyruvate AR carboxylase (PEPC; EC 4.1.1.31) are controlled posttranslationally by specific reversible phosphorylation of a strictly conserved serine residue near the N-terminus. This up/down-regulation of PEPC is catalyzed by a dedicated and highly regulated serine/threonine (Ser/Thr) kinase (PEPC-kinase) and an opposing type-2A Ser/Thr phosphatase (PP2A). In marked contrast to PEPC-kinase, the PP2A holoenzyme from photosynthetic tissue has been virtually unstudied to date. In the present investigation, we have partially purified and characterized the native form of this PP2A from illuminated leaves of maize (Zea mays L.), a C4 plant, using maize [32P]PEPC as substrate. Various conventional chromatographic matrices, together with thiophosphorylated C4 PEPC-peptide and microcystin-LR affinity-supports, were exploited for the enrichment of this PP2A from soluble leaf extracts. Biochemical and immunological results indicate that the C4-leaf holoenzyme is analogous to other eukaryotic PP2As in being a approximately 170-kDa heteromer comprised of a core PP2Ac-A heterodimer (approximately 38- and approximately 65-kDa subunits, respectively) complexed with a putative, approximately 74-kDa B-type regulatory/targeting subunit. This heterotrimer lacks any strict substrate specificity in that it dephosphorylates C4 PEPC, mammalian phosphorylase a, and casein in vitro. This activity is independent of free Me2+, insensitive to levamisole and the Inhibitor-2 protein that targets PP1, activated by several polycations such as protamine and poly-L-lysine, and highly sensitive to inhibition by microcystin-LR and okadaic acid (IC50 approximately 30 pM), all of which are diagnostic features of yeast and mammalian PP2As. In addition, this C4-leaf PP2A holoenzyme (i) is inhibited in vitro by physiological concentrations of certain C4 PEPC-related metabolites (L-malate, PEP, glucose 6-phosphate, but not the activator glycine) when either 32P-labeled maize PEPC or rabbit muscle

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phosphorylase a is used as substrate, suggesting a direct effect on this Ser/Thr phosphatase; and (ii) displays, at best, only modest light/dark effects in vivo on its apparent molecular mass, component core subunits and activity against C4 PEPC, in marked contrast to the opposing activity of PEPC-kinase in C4 and Crassulacean acid metabolism leaves. This report represents one of the few studies of a heteromeric PP2A holoenzyme from photosynthetic tissue that dephosphorylates a known target enzyme in plants, such as PEPC, sucrose-phosphate synthase or nitrate reductase.

L74 ANSWER 3 OF 31 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.

2001:244984 BIOSIS ACCESSION NUMBER: DOCUMENT NUMBER: PREV200100244984

TITLE: Mutations in yeast protein phosphatase

type 1 that affect targeting subunit binding.

AUTHOR(S): Wu, Xiaolin (1); Tatchell, Kelly (1)

(1) LSU Health Science Center, 1501 Kings Highway, CORPORATE SOURCE:

Shreveport, LA, 71130 USA

FASEB Journal, (March 7, 2001) Vol. 15, No. 4, pp. All. SOURCE:

Meeting Info.: Annual Meeting of the Federation of American Societies for Experimental Biology on Experimental Biology

2001 Orlando, Florida, USA March 31-April 04, 2001

ISSN: 0892-6638.

DOCUMENT TYPE: Conference LANGUAGE: English SUMMARY LANGUAGE: English

The activity of protein phosphatase 1 (PP1) is

controlled by targeting subunits, many of which are though to bind to a hydrophobic channel in PP1 via a short consensus sequence termed the VxF motif. Eleven mutants were constructed in the gene encoding budding yeast PP1 (GLC7) in which one or more of the residues comprising the hydrophobic channel were changed to alanine. These mutants were tested for biological and biochemical activity, and for their ability to associate with three PP1 binding proteins. All eleven mutants were

expressed in yeast and found to retain phosphatase activity towards myelin

basic protein. However, many mutants were deficient in

phosphorylase a phosphatase activity and were

hypersensitive to trypsin digestion. Five of the eleven were unable to complement the lethality of a glc7::LEU2 deletion. Many of the mutants were deficient in **binding** VxF motif-containing targeting subunits that regulate glucose repression and glycogen accumulation (Gaclp and Reglp) but all retained the ability to associate with Sds22p, a regulatory subunit that lacks this motif. The subcellular locations at which Glc7p normally accumulates (bud neck, nucleolus, spindle pole body) were missing in several of the mutants. Together, these results demonstrate the importance of the hydrophobic channel for regulating many cellular pathways and for the proper subcellular localization of Glc7p. The lack of phosphorylase a

phosphatase activity and trypsin-sensitivity in many of the mutants $% \left(1\right) =\left(1\right) \left(1\right) +\left(1\right) \left(1\right) \left(1\right) +\left(1\right) \left(1$ suggests that the channel may not act solely as a binding site for regulatory subunits.

L74 ANSWER 4 OF 31 CAPLUS COPYRIGHT 2003 ACS ACCESSION NUMBER: 2000:161323 CAPLUS

DOCUMENT NUMBER: 132:204861

TITLE: Protein domains in the hepatic glycogen-targeting

subunit of protein phosphatase 1

and their use in modulation of blood glucose

levels

INVENTOR(S): Cohen, Patricia Townsend Wade; Armstrong, Christopher

George; Doherty, Martin John Medical Research Council, UK

PATENT ASSIGNEE(S): SOURCE:

PCT Int. Appl., 51 pp.

CODEN: PIXXD2

DOCUMENT TYPE: Patent LANGUAGE: English

FAMILY ACC. NUM. COUNT:

PATENT INFORMATION:

PATENT NO. KIND DATE APPLICATION NO. DATE

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WO 1999-GB2761 19990819
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        RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL,
            PT, SE
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                           20000309
                                          CA 1999-2340885 19990819
     CA 2340885
                                          AU 1999-54368
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                      A1
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    EP 1107986
                           20010620
                      A1
        R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT,
            IE, FI
                                          JP 2000-567566 19990819
     JP 2002532381
                      T2
                           20021002
PRIORITY APPLN. INFO.:
                                       GB 1998-18650 A 19980827
                                                       W 19990819
                                       WO 1999-GB2761
    Three functional domains are identified in the glycogen-targeting subunit
     (GL) of rat liver protein phosphatase 1. Amino acid
     residues 94-267 of GL are required for binding to glycogen, the
    phosphorylase a-binding site lies in the
     C-terminal 16 amino acids, and the protein phosphatase
     1-binding domain lies between residues 59 and 94. The present
     invention relates to to the C-terminal 16-amino acid domain
     (PEWPSYGYEKLYPYY) domain, which is useful for treating disorders assocd.
     with abnormal blood glucose levels in mammals, such as Type I
     and Type II diabetes. The invention also relates to methods of making and
     using the peptide and related compds. which block the interaction of
    phosphorylase a with GL of protein
    phosphatase 1.
REFERENCE COUNT:
                              THERE ARE 5 CITED REFERENCES AVAILABLE FOR THIS
                        5
                              RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT
1.74 ANSWER 5 OF 31
                       MEDITNE
                                                       DUPLICATE 3
ACCESSION NUMBER:
                   2001059043
                                  MEDLINE
DOCUMENT NUMBER:
                   20532645 PubMed ID: 11080185
TITLE:
                   Ischemia-induced phosphorylation of initiation factor 2 in
                   differentiated PC12 cells: role for initiation factor 2
                    phosphatase.
AUTHOR:
                   Munoz F; Martin M E; Manso-Tomico J; Berlanga J; Salinas M;
                   Fando J L
CORPORATE SOURCE:
                   Department of Biochemistry and Molecular Biology, Alcala
                   University, Madrid, Spain.
                    JOURNAL OF NEUROCHEMISTRY, (2000 Dec) 75 (6) 2335-45.
SOURCE:
                   Journal code: 2985190R. ISSN: 0022-3042.
PUB. COUNTRY:
                   United States
DOCUMENT TYPE:
                   Journal; Article; (JOURNAL ARTICLE)
LANGUAGE:
                   English
FILE SEGMENT:
                   Priority Journals
ENTRY MONTH:
                   200012
ENTRY DATE:
                   Entered STN: 20010322
                   Last Updated on STN: 20010322
                   Entered Medline: 20001228
    An in vitro model of ischemia was obtained by subjecting PC12 cells
     differentiated with nerve growth factor to a combination of
    glucose deprivation plus anoxia. Immediately after the ischemic
    period, the protein synthesis rate was significantly inhibited (80%) and
    western blots of cell extracts revealed a significant accumulation of
    phosphorylated eukaryotic initiation factor 2, alpha subunit, eIF2(alphaP)
     (42%). Upon recovery, eIF2(alphaP) levels returned to control values after
     30 min, whereas protein synthesis was still partially inhibited (33%) and
     reached almost control values within 2 h. The activities of the mammalian
     eIF2alpha kinases, double-stranded RNA-activated protein kinase, mammalian
     GCN2 homologue, and endoplasmic reticulum-resident kinase, were
     determined. None of the eIF2alpha kinases studied showed increased
     activity in ischemic cells as compared with controls. Exposure of cells to
     cell-permeable inhibitors of protein
    phosphatases 1 and 2A, calyculin A or tautomycin, induced dose-
     and time-dependent accumulation of eIF2(alphaP), mimicking an ischemic
     effect. Protein phosphatase activity, as measured with
     [(32)P]phosphorylase a as a substrate, diminished
    during ischemia and returned to control levels upon 30-min recovery. In
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addition, the rate of eIF2(alphaP) dephosphorylation was significantly lower in ischemic cells, paralleling both the greatest translational inhibition and the highest eIF2(alphaP) levels. The endogenous phosphatase

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activity from control and ischemic extracts showed different sensitivity to inhibitor 2 and fostriecin in in vitro assays, inhibitor-2 effect in ischemic cells being lower than in control cells. Together these results indicate that an eIF2alpha phosphatase, probably protein phosphatase 1, is implicated in the ischemia-induced eIF2(alphaP) accumulation in PC12 cells.

L74 ANSWER 6 OF 31 MEDLINE DUPLICATE 4

ACCESSION NUMBER: 2000504874 MEDLINE

DOCUMENT NUMBER: 20506746 PubMed ID: 11055555

TITLE: Reciprocal regulation of glycogen phosphorylase and

glycogen synthase by insulin involving phosphatidylinositol-

3 kinase and protein phosphatase-1 in

HepG2 cells.

AUTHOR: Syed N A; Khandelwal R L

CORPORATE SOURCE: Department of Biochemistry, University of Saskatchewan,

Saskatoon, Canada.

SOURCE: MOLECULAR AND CELLULAR BIOCHEMISTRY, (2000 Aug) 211 (1-2)

123-36.

Journal code: 0364456. ISSN: 0300-8177.

PUB. COUNTRY: Netherlands

DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

ENTRY MONTH:

200102

ENTRY DATE:

Entered STN: 20010322

Last Updated on STN: 20021218 Entered Medline: 20010215

The effect of insulin on glycogen synthesis and key enzymes of glycogen metabolism, glycogen phosphorylase and glycogen synthase, was studied in HepG2 cells. Insulin stimulated glycogen synthesis 1.83-3.30 fold depending on insulin concentration in the medium. Insulin caused a maximum of 65% decrease in glycogen phosphorylase 'a' and 110% increase in glycogen synthase activities in 5 min. Although significant changes in enzyme activities were observed with as low as 0.5 nM insulin level, the maximum effects were observed with 100 nM insulin. There was a significant inverse correlation between activities of glycogen phosphorylase 'a' and glycogen synthase 'a' (R2= 0.66, p < 0.001). Addition of 30 mM glucose caused a decrease in phosphorylase 'a' activity in the absence of insulin and this effect was additive with insulin up to 10 nM concentration. The inactivation of **phosphorylase 'a'** by insulin was prevented by wortmannin and rapamycin but not by PD98059. The activation of glycogen synthase by insulin was prevented by wortmannin but not by PD98059 or rapamycin. In fact, PD98059 slightly stimulated glycogen synthase activation by insulin. Under these experimental conditions, insulin decreased glycogen synthase kinase-3beta activity by 30-50% and activated more than 4-fold particulate protein

phosphatase- activity and 1.9-fold protein kinase B activity;
changes in all of these enzyme activities were abolished by wortmannin.
The inactivation of GSK-3beta and activation of PKB by insulin were
associated with their phosphorylation and this was also reversed by
wortmannin. The addition of protein phosphatase-1

inhibitors, okadaic acid and calyculin A, completely abolished the effects of insulin on both enzymes. These data suggest that stimulation of glycogen synthase by insulin in HepG2 cells is mediated through the PI-3 kinase pathway by activating PKB and PP-1G and inactivating GSK-3beta. On the other hand, inactivation of phosphorylase by insulin is mediated through the PI-3 kinase pathway involving a rapamycin-sensitive p70(s6k) and PP-1G. These experiments demonstrate that insulin regulates glycogen phosphorylase and glycogen synthase through (i) a common signaling pathway at least up to PI-3 kinase and bifurcates downstream and (ii) that PP-1 activity is essential for the effect of insulin.

L74 ANSWER 7 OF 31 MEDLINE DUPLICATE 5

ACCESSION NUMBER: 1999445266 MEDLINE

DOCUMENT NUMBER: 99445266 PubMed ID: 10517678

TITLE: Effect of an Asp905Tyr mutation of the glycogen-associated

regulatory subunit of protein phosphatase

-1 on the regulation of glycogen synthesis by insulin and

cyclic adenosine 3',5'-monophosphate agonists.

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AUTHOR: Ragolia L; Duddy N; Begum N

CORPORATE SOURCE: Diabetes Research Laboratory, Winthrop University Hospital,

Mineola, New York 11501, USA.

MOLECULAR ENDOCRINOLOGY, (1999 Oct) 13 (10) 1773-83.

Journal code: 8801431. ISSN: 0888-8809.

United States PUB. COUNTRY:

DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

ENTRY MONTH: 199912

ENTRY DATE: Entered STN: 20000113

Last Updated on STN: 20000113 Entered Medline: 19991222

The glycogen-associated regulatory subunit of protein phosphatase-1 (PP-1G) plays a major role in insulin-stimulated glycogen synthesis and thus the regulation of nonoxidative glucose disposal in skeletal muscle. In a general population of Caucasians a polymorphism at codon 905 of PP-1G from an aspartate to tyrosine has been reported to be associated with insulin resistance and hypersecretion. In this report functional studies were performed on rat skeletal muscle L6 cells stably transfected with an Asp905Tyr mutant PP-1G to evaluate the impact of this mutation on cellular responsiveness to insulin and cAMP. Although transfection resulted in a 3-fold increase in mutant PP-1G subunit expression, basal and insulin-stimulated PP-1 catalytic activities were decreased when compared with L6 cells transfected with wild-type PP-1G. The Asp905Tyr mutation resulted in an increase in cellular sensitivity to cAMP agonist, resulting in an inhibition of insulin's stimulatory effect on glycogen synthesis. More importantly, low concentrations of (Bu)2cAMP completely reversed insulin's stimulatory effects on glycogen synthesis when added to insulin-treated cells expressing mutant PP-1G. This was due to a rapid activation of glycogen phosphorylase a and a simultaneous inactivation of glycogen synthase via cAMP-mediated reductions in insulin-stimulated PP-1 catalytic activities. We conclude that an Asp905Tyr mutation of PP-1G is accompanied by a relative increase in sensitivity to cAMP agonists as well as a diminished capacity of the mutant PP-1G to effectively mediate the inhibitory effects of insulin on glycogen breakdown via PP-1 activation.

L74 ANSWER 8 OF 31 MEDLINE DUPLICATE 6

ACCESSION NUMBER: 1999348016 MEDLINE

DOCUMENT NUMBER: 99348016 PubMed ID: 10417316

TITLE: Influence of substrates on in vitro dephosphorylation of

> glycogen phosphorylase a by protein phosphatase-1.

AUTHOR -Wang Z X

CORPORATE SOURCE: National Laboratory of Biomacromolecules, Institute of

Biophysics, Academia Sinica, Beijing 100101, People's

Republic of China.. zxwang@sun5.ibp.ac.cn

BIOCHEMICAL JOURNAL, (1999 Aug 1) 341 (Pt 3) 545-54. SOURCE:

Journal code: 2984726R. ISSN: 0264-6021.

ENGLAND: United Kingdom PUB COUNTRY:

DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

ENTRY MONTH: 199909

Entered STN: 19990925 ENTRY DATE:

> Last Updated on STN: 19990925 Entered Medline: 19990916

The kinetic theory of the substrate reaction during modification of enzyme activity has been applied to a study of the dephosphorylation of phosphorylase a by protein phosphatase

-1 (ppase-1). On the basis of the kinetic equation of the substrate reaction in the presence of ppase-1, all the inactivation rate constants for the free enzyme and the enzyme-substrate(s) complexes have been determined. Binding of the allosteric substrate, glucose 1-phosphate, to one subunit of phosphorylase a

protects completely against ppase-1 action on either the same subunit or the adjacent subunit, whereas binding of the non-allosteric substrate, glycogen, to one subunit protects this subunit partially, but has no effect on the modification on the neighbouring subunit. Analysis of

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the data suggests that the allosteric behaviour of phosphorylase a can be interpreted in terms of a modified concerted model. The present method also provides a novel approach for studying dephosphorylation reactions. Since the experimental conditions used resemble more closely the in vivo situation where the substrate is constantly being turned over while the enzyme is being modified, this new method would be particularly useful when the regulatory mechanism of the reversible phosphorylation reaction toward certain enzymes is being assessed.

L74 ANSWER 9 OF 31 SCISEARCH COPYRIGHT 2003 ISI (R)

1999:752467 SCISEARCH ACCESSION NUMBER:

THE GENUINE ARTICLE: 240VT

TITLE:

Inhibition of glycogenolysis in primary rat hepatocytes by

1,4-dideoxy-1,4-imino-d-arabinitol

AUTHOR: Andersen B (Reprint); Rassov A; Westergaard N; Lundgren K NOVO NORDISK AS, DEPT DIABET BIOCHEM & METAB, BLDG C9-S19, CORPORATE SOURCE:

NOVO NORDISK PK, DK-2760 MALOV, DENMARK (Reprint)

COUNTRY OF AUTHOR: DENMARK

BIOCHEMICAL JOURNAL, (15 SEP 1999) Vol. 342, Part 3, pp.

545-550.

Publisher: PORTLAND PRESS, 59 PORTLAND PLACE, LONDON WIN

3AJ, ENGLAND. ISSN: 0264-6021. Article; Journal

FILE SEGMENT: LIFE

DOCUMENT TYPE:

SOURCE:

LANGUAGE: English REFERENCE COUNT:

ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

1,4-Dideoxy-1,4-imino-D-arabinitol (DAB) was identified previously-as a potent inhibitor of both the phosphorylated and non-phosphorylated forms of glycogen phosphorylase (EC 2.4.1.1). In the present study, the effects of DAB were investigated in primary cultured rat hepatocytes. The transport of DAB into hepatocytes was dependent on time and DAB concentration. The rate of DAB transport was 192 pmol/min per mg of protein per mM DAB(medium-concentration). In hepatocytes, DAB inhibited basal and glucagon-stimulated glycogenolysis with IC50 values of 1.0 +/- 0.3 and 1.1 +/- 0.2 mu M, respectively. The primary inhibitory effect of DAB on glycogenolysis was shown to be due to inhibition of glycogen phosphorylase but, at higher concentrations of DAB, inhibition of the debranching enzyme (4-alpha-glucanotransferase, EC 2.4.1.25) may have an effect. No effects on glycogen synthesis were observed, demonstrating that glycogen recycling does not occur in cultured hepatocytes under the conditions tested. Furthermore, DAB had no effects on phosphorylase kinase, the enzyme responsible for phosphorylation and thereby activation of glycogen phosphorylase, or on protein phosphatase 1, the enzyme responsible for inactivation of glycogen phosphorylase

through dephosphorylation.

L74 ANSWER 10 OF 31 CAPLUS COPYRIGHT 2003 ACS DUPLICATE 7

ACCESSION NUMBER: 1999:360581 CAPLUS

DOCUMENT NUMBER: 131:166946

TITLE: Role of the 78-kDa Glucose-Regulated Protein

as an Activity Modulator of Protein

Phosphatasel.gamma.2

Chun, Yang-Sook; Park, Jong-Wan; Kim, Myung-Suk; AUTHOR(S):

Shima, Hiroshi; Nagao, Minako; Lee, Seung-Hoon; Park,

Sang-Woon; Chung, Myung-Hee

CORPORATE SOURCE: Department of Pharmacology, Seoul National University,

College of Medicine, Seoul, 110-799, S. Korea

Biochemical and Biophysical Research Communications (1999), 259(2), 300-304

CODEN: BBRCA9; ISSN: 0006-291X

PUBLISHER: Academic Press DOCUMENT TYPE: Journal LANGUAGE: English

We have previously found the 78-kDa glucose-regulated protein (Grp78) to be a subunit of protein phosphatasel (PP1).gamma.2. To det. the role of Grp78 in PP1.gamma.2 holoenzyme, we compared the two forms of this enzyme, PP1.gamma.2 holoenzyme contg. Grp78 and Grp78-dissocd. PP1.gamma.2 in rat testes in terms of their kinetic consts. and

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sensitivities to inhibitors of this enzyme. The enzymic activity of the Grp78-dissocd. enzyme was much lower at whole range of concns. of a substrate (phosphorylase a) than that of the holoenzyme; the Km value was about ten-fold higher in Grp78-dissocd. enzyme than in holoenzyme, while the Vmax was similar. IC50s of the Grp78-dissocd. enzyme for three inhibitors (microcystin-LR, inhibitor-2, and okadaic acid) were more than ten-fold higher than those of the holoenzyme. These results indicate that the Grp78 subunit modulates the activity of PP1.gamma.2 through its actions to control the binding of substrates or inhibitors to PP1.gamma.2. (c) 1999 Academic Press.

REFERENCE COUNT:

THERE ARE 29 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L74 ANSWER 11 OF 31 SCISEARCH COPYRIGHT 2003 ISI (R)

1998:344105 SCISEARCH ACCESSION NUMBER:

THE GENUINE ARTICLE: ZK620

Protein phosphatase-1 and insulin TITLE:

action

AUTHOR: Ragolia L; Begum N (Reprint)

CORPORATE SOURCE:

WINTHROP UNIV HOSP, DIABET RES LAB, 259 1ST ST, MINEOLA, NY 11501 (Reprint); WINTHROP UNIV HOSP, DIABET RES LAB, MINEOLA, NY 11501; SUNY STONY BROOK, SCH MED, STONY BROOK,

NY 11794

COUNTRY OF AUTHOR:

SOURCE:

MOLECULAR AND CELLULAR BIOCHEMISTRY, (MAY 1998) Vol. 182,

No. 1-2, pp. 49-58.

Publisher: KLUWER ACADEMIC PUBL, SPUIBOULEVARD 50, PO BOX

17, 3300 AA DORDRECHT, NETHERLANDS.

TSSN: 0300-8177. Article; Journal

DOCUMENT TYPE: FILE SEGMENT:

LIFE

LANGUAGE: English REFERENCE COUNT: 70

ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

Protein Phosphatase-1 (PP-1) appears to be the key component of the insulin signalling pathway which is responsible for bridging the initial insulin-simulated phosphorylation cascade with the ultimate dephosphorylation of insulin sensitive substrates. Dephosphorylations catalyzed by PP-1 activate glycogen synthase (GS) and simultaneously inactivate phosphorylase a and phosphorylase kinase promoting glycogen synthesis. Our in vivo studies using L6 rat skeletal muscle cells and freshly isolated adipocytes indicate that insulin stimulates PP-1 by increasing the phosphorylation status of its regulatory subunit (PP-1(G)). PP-1 activation is accompanied by an inactivation of Protein Phosphatase-2A (PP-2A) activity. To gain insight into the upstream kinases that mediate insulin-stimulated PP-1(G) phosphorylation, we employed inhibitorsof the ras/MAPK, PI3-kinase, and PKC signalling pathways. These inhibitor studies suggest that PP-1, phosphorylation is mediated via a complex, cell type specific mechanism involving PI3-kinase/PKC/PKB and/or the ras/MAP kinase/Rsk kinase cascade. CAMP agonists such as SpcAMP (via PKA) and TNF-alpha (recently identified as endogenous inhibitor of insulin action via ceramide) block insulin-stimulated PP-1(G) phosphorylation with a parallel decrease of PP-1 activity, presumably due to the dissociation of the PP-1 catalytic subunit from the regulatory G-subunit. It appears that any agent or condition which interferes with the insulin-induced phosphorylation and activation of PP-1, will decrease the magnitude of insulin's effect on downstream metabolic processes. Therefore, regulation of the PP-1(G) subunit by site-specific phosphorylation plays an important role in insulin signal transduction in target cells. Mechanistic and functional studies with cell lines expressing PP-1(G) subunit site-specific mutations will help clarify

L74 ANSWER 12 OF 31 MEDLINE

PP-1 catalytic function.

DUPLICATE 8

ACCESSION NUMBER:

97197908 MEDLINE

DOCUMENT NUMBER: TITLE:

PubMed ID: 9045612 97197908 PTG, a protein phosphatase 1-

binding protein with a role in glycogen metabolism.

the exact role and regulation of PP-1(G) site-specific phosphorylations on

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Printen J A; Brady M J; Saltiel A R AUTHOR:

CORPORATE SOURCE: Department of Physiology, University of Michigan School of

Medicine, Ann Arbor, MI 48109, USA.

SCIENCE, (1997 Mar 7) 275 (5305) 1475-8. SOURCE:

Journal code: 0404511. ISSN: 0036-8075.

United States PUB. COUNTRY:

DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)

English LANGUAGE:

FILE SEGMENT: Priority Journals GENBANK-U89924 OTHER SOURCE:

ENTRY MONTH: 199703

ENTRY DATE: Entered STN: 19970407

> Last Updated on STN: 19970407 Entered Medline: 19970326

Protein dephosphorylation by phosphatase PPI plays a central role in mediating the effects of insulin on glucose and lipid metabolism. A PP1C-targeting protein expressed in 3T3-L1 adipocytes (called PTG, for protein targeting to glycogen) was cloned and characterized. PTG was expressed predominantly in insulin-sensitive tissues. In addition to binding and localizing PPIC to glycogen, PTG formed complexes with phosphorylase kinase, phosphorylase a, and glycogen synthase, the primary enzymes involved in the hormonal regulation of glycogen metabolism. Overexpression of PTG markedly increased basal and insulin-stimulated glycogen synthesis in Chinese hamster ovary cells overexpressing the insulin receptor, which do not express endogenous PTG. These results suggest that PTG is critical for glycogen metabolism, possibly functioning as a molecular scaffold.

MEDLINE DUPLICATE 9 L74 ANSWER 13 OF 31

ACCESSION NUMBER: 97220381 MEDLINE

DOCUMENT NUMBER: 97220381 PubMed ID: 9148744

TITLE:

Glucose-induced glycogenesis in the liver involves the glucose-6-phosphate-dependent

dephosphorylation of glycogen synthase.

AUTHOR: Cadefau J; Bollen M; Stalmans W

Afdeling Biochemie, Faculteit Geneeskunde, Katholieke CORPORATE SOURCE:

Universiteit Leuven, Herestraat 49, B-3000 Leuven, Belgium.

BIOCHEMICAL JOURNAL, (1997 Mar 15) 322 (Pt 3) 745-50. SOURCE:

Journal code: 2984726R. ISSN: 0264-6021.

ENGLAND: United Kingdom PUB. COUNTRY:

DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

ENTRY MONTH: 199705

ENTRY DATE: Entered STN: 19970523

Last Updated on STN: 19970523 Entered Medline: 19970509

Non-metabolized glucose derivatives may cause inactivation of phosphorylase but, unlike glucose, they are unable to elicit activation of glycogen synthase in isolated hepatocytes. We report here that, after the previous inactivation of phosphorylase by one of these glucose derivatives (2-deoxy-2-fluoro-alpha-glucosyl fluoride), glycogen synthase was progressively activated by addition of increasing concentrations of glucose. Under these conditions, the degree of activation of glycogen synthase was linearly correlated with the intracellular glucose-6-phosphate (Glc-6-P) concentration. Addition of glucosamine, an inhibitor of glucokinase, decreased both parameters in parallel. Further experiments using an inhibitor of either protein kinases (5-iodotubercidin) or protein phosphatases (microcystin) in isolated hepatocytes indicated that Glc-6-P does not affect glycogen-synthase kinase activity but enhances the glycogen-synthase phosphatase reaction. Experiments in vitro showed that the synthase phosphatase activity of glycogen-bound type-1 protein phosphatase was increased by physiological concentrations of Glc-6-P (0.1-0.5 mM), but not by 2.5 mM fructose-6-P, fructose-1-P or glucose-1-P. At physiological ionic strength, the glycogen-associated synthase phosphatase activity was nearly entirely Glc-6-P-dependent, but Glc-6-P did not relieve the strong inhibitory effect of phosphorylase a

. The large stimulatory effects of 2.5 mM Glc-6-P, with glycogen synthase b and phosphorylase a as substrates, appeared to be

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mostly substrate-directed, while the modest effects observed with casein and histone IIA pointed to an additional stimulation of glycogen-bound protein phosphatase-1 by Glc-6-P. We conclude that glucose elicits hepatic synthase phosphatase activity both by removal of the inhibitor, phosphorylase a, and by generation of the stimulator, Glc-6-P.

L74 ANSWER 14 OF 31 SCISEARCH COPYRIGHT 2003 ISI (R)

ACCESSION NUMBER: 95:825923 SCISEARCH

THE GENUINE ARTICLE: TG087

TITLE: INVOLVEMENT OF PHOSPHORYLASE-KINASE INHIBITION IN THE

EFFECT OF RESORCINOL AND PROGLYCOSYN ON

GLYCOGEN-METABOLISM IN THE LIVER

AUTHOR: VANSCHAFTINGEN E (Reprint)

CORPORATE SOURCE: UNIV CATHOLIQUE LOUVAIN, CHIM PHYSIOL LAB, 75 AVE

HIPPOCRATE, B-1200 BRUSSELS, BELGIUM (Reprint); INT INST

CELLULAR & MOLEC PATHOL, BRUSSELS, BELGIUM

COUNTRY OF AUTHOR: BELGIUM

SOURCE: EUROPEAN JOURNAL OF BIOCHEMISTRY, (15 NOV 1995) Vol. 234,

No. 1, pp. 301-307.

ISSN: 0014-2956. Article; Journal

DOCUMENT TYPE: Article FILE SEGMENT: LIFE

LANGUAGE: ENGLISH REFERENCE COUNT: 31

ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

The purpose of this study was to identify the mechanism by which proglycosyn and resorcinol decrease the **phosphorylase a** content and the fructose 2,6-bisphosphate concentration in isolated hepatocytes. The intracellular concentrations of the glucuronide derivatives of proglycosyn and resorcinol have been measured by HPLC in hepatocytes incubated for 5 min or 30 min with different concentrations of these agents. At both times, there was a reciprocal relationship between the **phosphorylase a** content and the intracellular concentration of the glucuronidated metabolites, half-maximal inactivation being observed at about 2 mu lmol/g protein and 0.25 mu mol/g protein for resorcinylglucuronide and proglycosyn-glucuronide, respectively. Glycogen

synthase was not significantly activated by these agents after 5 min but was well activated after 30 min.

Preincubation of hepatocytes with 1 mM resorcinol or with 100 mu M proglycosyn resulted in a decrease in the rate at which phosphorylase was

activated following the addition of glucagon, vasopressin, the **protein phosphatase inhibitor** calyculin A or the calcium ionophore A 23187, but did not reduce the rate of synthase inactivation. Proglycosynglucuronide and resorcinylglucuronide inhibited phosphorylase kinase in liver Sephadex filtrates, with K-i values of about 0.75 mM and 4 mM, respectively. Preincubation of the filtrates with ATP and cAMP decreased the sensitivity of phosphorylase kinase to resorcinylglucuronide by about fourfold. It is concluded that the effect of resorcinol and proglycosyn on the **phosphorylase** a content is due, at least partly, to an inhibition of phosphorylase kinase by their glucuronidated metabolites.

Resorcinol and proglycosyn caused a parallel decrease in the concentration of fructose 2,6-bisphosphate and of hexose 6-phosphates, without significantly changing the activity of 6-phosphofructo-2-kinase. The decrease in the fructose 2,6-bisphosphate concentration appears therefore to be secondary to the decrease in the hexose 6-phosphate concentration.

L74 ANSWER 15 OF 31 MEDLINE DUPLICATE 10

ACCESSION NUMBER: 94235641 MEDLINE

DOCUMENT NUMBER: 94235641 PubMed ID: 8180201

TITLE: Design of inhibitors of glycogen

phosphorylase: a study of alpha- and

beta-C-glucosides and 1-thio-beta-D-glucose

compounds.

AUTHOR: Watson K A; Mitchell E P; Johnson L N; Son J C; Bichard C

J; Orchard M G; Fleet G W; Oikonomakos N G; Leonidas D D;

Kontou M; +

CORPORATE SOURCE: Oxford Centre for Molecular Sciences, U.K.

SOURCE: BIOCHEMISTRY, (1994 May 17) 33 (19) 5745-58.

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Journal code: 0370623. ISSN: 0006-2960.

PUB. COUNTRY: United States

DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

ENTRY MONTH: 199406

ENTRY DATE: Entered STN: 19940621

Last Updated on STN: 19980206 Entered Medline: 19940616

alpha-D-Glucose is a weak inhibitor of glycogen phosphorylase b (Ki = 1.7 mM) and acts as a physiological regulator of hepatic glycogen metabolism. Glucose binds to phosphorylase at the catalytic site and results in a conformational change that stabilizes the inactive T state of the enzyme, promoting the action of protein phosphatase 1 and stimulating glycogen synthase. It has been suggested that, in the liver, glucose analogues with greater affinity for glycogen phosphorylase may result in a more effective regulatory agent. Several alpha- and betaanhydroglucoheptonic acid derivatives and 1-deoxy-1-thio-beta-Dglucose analogues have been synthesized and tested in a series of crystallographic and kinetic binding studies with glycogen phosphorylase. The structural results of the bound enzyme-ligand complexes have been analyzed, together with the resulting affinities, in an effort to understand and exploit the molecular interactions that might give rise to a better inhibitor. This work has shown the following: (i) Similar affinities may be obtained through different sets of interactions. Specifically, in the case of the alpha- and beta-glucose -C-amides, similar Ki's (0.37 and 0.44 mM, respectively) are obtained with the alpha-anomer through interactions from the ligand via water molecules to the protein and with the beta-anomer through direct interaction from the ligand to the protein. Thus, hydrogen bonds through water can contribute binding energy similar to that of hydrogen bonds directly to the protein. (ii) Attempts to improve the inhibition by additional groups did not always lead to the expected result. The addition of nonpolar groups to the alpha-carboxamide resulted in a change in conformation of the pyranose ring from a chair to a skew boat and the consequent loss of favorable hydrogen bonds and increase in the Ki. (iii) The addition of polar groups to the alpha-carboxamide led to compounds with the chair conformation, and in the examples studied, it appears that hydration by a water molecule may provide sufficient stabilization to retain the chair conformation. (iv) The best inhibitor was N-methyl-beta-glucose-C-carboxamide (Ki = 0.16 mM), which showed a 46-fold improvement in Ki from the parent beta-D-glucose. The decrease in Ki may be accounted for by a single hydrogen bond from the amide nitrogen to a main-chain carbonyl oxygen, an increase in entropy through displacement of a water molecule, and favorable van der Waals

L74 ANSWER 16 OF 31 SCISEARCH COPYRIGHT 2003 ISI (R)

residues. (ABSTRACT TRUNCATED AT 250 WORDS)

ACCESSION NUMBER: 94:224555 SCISEARCH

THE GENUINE ARTICLE: NF816

TITLE: IDENTIFICATION OF THE GLYCOGENIC COMPOUND 5-IODOTUBERCIDIN

contacts between the methyl substituent and nonpolar protein

AS A GENERAL PROTEIN-KINASE INHIBITOR

AUTHOR: MASSILLON D; STALMANS W (Reprint); VANDEWERVE G; BOLLEN M CORPORATE SOURCE: CATHOLIC UNIV LEUVEN, FAK GENEESKUNDE, AFDELING BIOCHEM,

HERESTR 49, B-3000 LOUVAIN, BELGIUM (Reprint); CATHOLIC UNIV LEUVEN, FAK GENEESKUNDE, AFDELING BIOCHEM, B-3000 LOUVAIN, BELGIUM; UNIV MONTREAL, DEPT NUTR, ENDOCRINOL METAB LAB, MONTREAL H3C 3J7, PQ, CANADA; UNIV MONTREAL, DEPT BIOCHEM, ENDOCRINOL METAB LAB, MONTREAL H3C 3J7, PQ,

CANADA

COUNTRY OF AUTHOR: BELGIUM; CANADA

SOURCE: BIOCHEMICAL JOURNAL, (01 APR 1994) Vol. 299, Part 1, pp.

123-128.

ISSN: 0264-6021.

DOCUMENT TYPE: Article; Journal

FILE SEGMENT: LIFE
LANGUAGE: ENGLISH
REFERENCE COUNT: 37

ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

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AR Addition of micromolar concentrations of the adenosine derivative 5-iodotubercidin (Itu) initiates glycogen synthesis in isolated hepatocytes by causing inactivation of phosphorylase and activation of glycogen synthase (Fluckiger-Isler and Waiter (1993) Biochem. J. 292, 85-91]. We report here that Itu also antagonizes the effects of saturating concentrations of glucagon and vasopressin on these enzymes. The Itu-induced activation of glycogen synthase could not be explained by the removal of phosphorylase a (a potent inhibitor of the glycogen-associated synthase phosphatase). When tested on purified enzymes, Itu did not affect the activities of the major Ser/Thr-specific protein phosphatases (PP-1, PP-2A, PP-2B and PP-2C), but it inhibited various Ser/Thr-specific protein kinases as well as the tyrosine kinase activity of the insulin receptor (IC50 between 0.4 and 28 mu M at 10-15 mu M ATP), Tubercidin, which did not affect glycogen synthase or phosphorylase in liver cells, was 300 times less potent as a protein kinase inhibitor. Kinetic analysis of the inhibition of casein kinase-1 and protein kinase A showed that Itu acts as a competitive inhibitor with respect to ATP, and as a mixed-type inhibitor with respect to the protein substrate. We propose that Itu inactivates phosphorylase and activates glycogen synthase by inhibiting phosphorylase kinase and various glycogen synthase kinases. Consistent with the broad specificity of Itu in vitro, this compound decreased the phosphorylation level of numerous phosphopolypeptides in intact liver cells. Our data suggest that at least some of the biological effects of Itu can be explained by an inhibition of protein kinases.

L74 ANSWER 17 OF 31 MEDLINE

ACCESSION NUMBER: 94324473

MEDLINE

DOCUMENT NUMBER: 94324473 PubMed ID: 8048502

TITLE: Phenylarsine oxide inhibits insulin-stimulated

protein phosphatase 1 activity and GLUT-4

translocation.

AUTHOR: Beaum N

Diabetes Research Laboratory, Winthrop University Hospital, CORPORATE SOURCE:

Mineola 11501.

SOURCE: AMERICAN JOURNAL OF PHYSIOLOGY, (1994 Jul) 267 (1 Pt 1)

E14-23.

Journal code: 0370511. ISSN: 0002-9513.

PUB. COUNTRY: United States

DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

ENTRY MONTH: 199408

ENTRY DATE: Entered STN: 19940909

Last Updated on STN: 19940909 Entered Medline: 19940830

AR Phenylarsine oxide (PAO) has previously been shown to inhibit insulin-stimulated glucose transport without affecting insulin binding and tyrosine kinase activity of insulin receptor (S. C. Frost and M. D. Lane. J. Biol. Chem. 260: 2646-2652, 1985). This study examines the effect of PAO on insulin's ability to activate adipocyte protein phosphatase 1 (PP-1) and dephosphorylate GLUT-4, the insulin-sensitive glucose transporter. In particulate fractions, insulin stimulated PP-1 activity (40% increase over basal with phosphorylase a) in a time- and dose-dependent manner (half-maximal effect of 0.89 nM in 1 min). Insulin did not alter cytosolic PP-1 activity. With GLUT-4 as a substrate, insulin caused more than twofold stimulation of particulate PP-1 activity. Addition of PAO (5 microM) before or after insulin treatment abolished insulin's effect on PP-1 activation. The presence of 2,3-dimercaptopropanol (200 microM) prevented the effect of PAO on PP-1 activation and glucose uptake. In addition, PAO significantly increased GLUT-4 phosphorylation, blocked insulin-stimulated dephosphorylation, and partially diminished insulin-stimulated translocation of GLUT-4. We conclude that PAO may interfere with the components of insulin signal transduction pathways that lead to the activation of PP-1 and this may be responsible for the observed inhibition in insulin action.

L74 ANSWER 18 OF 31 SCISEARCH COPYRIGHT 2003 ISI (R) ACCESSION NUMBER: 93:238633 SCISEARCH

THE GENUINE ARTICLE: KW979

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, Viv. TITLE:

MECHANISM OF IMPAIRED METABOLIC SIGNALING BY A TRUNCATED

HUMAN INSULIN-RECEPTOR - DECREASED ACTIVATION OF

PROTEIN PHOSPHATASE-1 BY INSULIN

AUTHOR:

BEGUM N; OLEFSKY J M; DRAZNIN B (Reprint)

CORPORATE SOURCE:

VET AFFAIRS MED CTR, DEPT MED, ENDOCRINOL SECT 111H, 1055 CLERMONT ST, DENVER, CO, 80220; VET AFFAIRS MED CTR, RES SERV, DENVER, CO, 80220; UNIV COLORADO, HLTH SCI CTR, DENVER, CO, 80220; UNIV CALIF SAN DIEGO, SCH MED, DEPT MED, LA JOLLA, CA, 92063; SAN DIEGO VET AFFAIRS MED CTR,

LA JOLLA, CA, 92063

COUNTRY OF AUTHOR:

SOURCE:

JOURNAL OF BIOLOGICAL CHEMISTRY, (15 APR 1993) Vol. 268,

No. 11, pp. 7917-7922.

ISSN: 0021-9258. Article; Journal

DOCUMENT TYPE: FILE SEGMENT:

LIFE ENGLISH

LANGUAGE:

48

USA

REFERENCE COUNT:

ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB Previous studies have shown that a human insulin receptor lacking the COOH-terminal 43-amino acid domain (HIRDELTACT) displays a compromised ability to stimulate glucose transport and glycogen synthase, whereas mitogenic signaling and stimulation of the insulin receptor tyrosine kinase activity remain intact (Maegawa, H., McClain, D. A., Freidenberg, G., Olefsky, J. M., Napier, M., Lipari, T., Dull, T. J., Lee, J., and Ullrich, A. (1988) J. Biol. Chem. 263, 8912-8917). In this study, we examined the effect of insulin on protein phosphatase 1 (PP-1) activity and phosphorylation in cells expressing wild-type human insulin receptor (HIRc) and HIRDELTACT cells using phosphorylase a as substrate in the presence of 3 nM okadaic acid. Basal PP-1 activity was significantly lower in HIRDELTACT than in HIRc cells (p <0.05). Insulin stimulated PP-1 activity in HIRc cells (25-30% increase over basal activity) in a time- and dose-dependent manner. Insulin failed to stimulate PP-1 activity in HIRDELTACT cells. Western blotting with the catalytic subunit antibody and the regulatory subunit antibody revealed similar amounts of the 37-kDa band (catalytic subunit) and the 160-kDa band (presumed regulatory subunit) in HIRc and HIRDELTACT cells. We conclude that the COOH-terminal domain of the insulin receptor is an important element in mediating the effect of insulin on PP-1 and suggest that activation of PP-1 may be linked to signaling insulin's metabolic actions.

L74 ANSWER 19 OF 31 SCISEARCH COPYRIGHT 2003 ISI (R)

ACCESSION NUMBER: 92:188545 SCISEARCH

THE GENUINE ARTICLE: HK318

TITLE:

CALCIUM-INDUCED INHIBITION OF PHOSPHOSERINE PHOSPHATASE IN

INSULIN TARGET-CELLS IS MEDIATED BY THE PHOSPHORYLATION

AND ACTIVATION OF INHIBITOR-1

AUTHOR: CORPORATE SOURCE: BEGUM N; SUSSMAN K E; DRAZNIN B (Reprint)

VET AFFAIRS MED CTR, MED RES SERV, ENDOCRINOL SECT 111H, 1055 CLERMONT ST, DENVER, CO, 80220; UNIV COLORADO, HLTH

SCI CTR, DEPT MED, DENVER, CO, 80262

COUNTRY OF AUTHOR:

SOURCE:

JOURNAL OF BIOLOGICAL CHEMISTRY, (25 MAR 1992) Vol. 267,

No. 9, pp. 5959-5963.

ISSN: 0021-9258.

DOCUMENT TYPE:

Article; Journal

FILE SEGMENT: LANGUAGE:

LIFE ENGLISH

REFERENCE COUNT:

ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

In this study, we examined the mechanism of inhibition of phosphoserine phosphatase (PSPase) activity by elevated [Ca2+]i in insulin target cells. In in vitro studies, isolated rat adipocytes were incubated with either 40 mM K+ or parathyroid hormone (PTH) (20 ng/ml) for 1 h. In in vivo studies, rats were injected with PTH (three hourly injections of 40-mu-g intraperitoneally) prior to isolation of either adipocytes or skeletal muscle. Under these conditions, intracellular [Ca2+]i changed from 100 +/-8.7 to 263 +/- 10.5 nM. There was a concomitant 30% decrease in adipocyte PSPase activity and a 35% decrease in skeletal muscle PSPase activity, assayed using P-32-labeled phosphorylase "a" as a

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substrate. The inhibition of PSPase was accompanied by a 60% increase in adipocytes (p < 0.05) and a 118% increase (p < 0.01) in skeletal muscle inhibitor 1 (I1) activities, respectively. Since Il is active only in the phosphorylated state, we studied the effect of [Ca2+]i on I1 phosphorylation. Sodium dodecyl sulfate-polyacrylamide gel electrophoresis of heat treated extracts immunoprecipitated with I1 antibody revealed significant increase in P-32 incorporation (45-60%, p < 0.05) into I1 protein in cells with elevated [Ca2+]i. Nitrendipine, a calcium channel blocker, completely prevented increases in I1 phosphorylation and activity in cells exposed to K+ but was only partially effective in the PTH-treated cells. In contrast, a cyclic AMP antagonist, RpcAMP, prevented both the K+- and the PTH-induced increases in Il phosphorylation and activity, even though it failed to block the elevations in [Ca2+]i in these cells. We conclude that [Ca2+]i-induced and cAMP-mediated phosphorylation and activation of Il results in inhibition of PSPase activity in insulin target cells. The inhibition of PSPases may cause inappropriate serine dephosphorylation of substrates of insulin action resulting in insulin resistance.

L74 ANSWER 20 OF 31 MEDLINE DUPLICATE 12

ACCESSION NUMBER: 92368355 MEDLINE

DOCUMENT NUMBER: 92368355 PubMed ID: 1323965

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TITLE: Effects of fructose 2,6-bisphosphate and glucose

1,6-bisphosphate on porcine heart protein

phosphatase 2A.

AUTHOR: Erickson A K; Killilea S D

CORPORATE SOURCE: Department of Biochemistry, North Dakota State University,

Fargo 58105.

SOURCE: BIOCHEMISTRY INTERNATIONAL, (1992 Jul) 27 (2) 353-9.

Journal code: 8100311. ISSN: 0158-5231.

PUB. COUNTRY: Australia

DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

ENTRY MONTH: 199209

ENTRY DATE: Entered STN: 19920925

Last Updated on STN: 19920925 Entered Medline: 19920916

AB Fructose 2,6-bisphosphate and glucose 1,6-bisphosphate are apparent noncompetitive inhibitors of porcine protein phosphatase 2A2 having Ki values of 0.38 and 0.56 mM,

respectively. The inhibitory effects were on the catalytic subunit and were not substrate directed. In addition, fructose 2,6-bisphosphate caused a time-dependent inactivation of phosphatase activity toward

phosphorylase a. This inactivation was antagonized by

MnCl2. The fructose 2,6-bisphosphate-inactivated enzyme had increased p-nitrophenyl phosphate phosphatase activity. These effects are similar to the known effects of ATP on type 2A phosphatases.

L74 ANSWER 21 OF 31 MEDLINE DUPLICATE 13

ACCESSION NUMBER: 91040667 MEDLINE

DOCUMENT NUMBER: 91040667 PubMed ID: 2122108

TITLE: Mechanisms of blood glucose homeostasis.

AUTHOR: Hers H G

CORPORATE SOURCE: Laboratoire de Chimie Physiologique, Universite Catholique

de Louvain, Brussels, Belgium.

SOURCE: JOURNAL OF INHERITED METABOLIC DISEASE, (1990) 13 (4)

395-410. Ref: 25

Journal code: 7910918. ISSN: 0141-8955.

PUB. COUNTRY: Netherlands

DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)

General Review; (REVIEW)

(REVIEW, TUTORIAL)

LANGUAGE: English

FILE SEGMENT: Priority Journals

ENTRY MONTH: 199012

ENTRY DATE: Entered STN: 19910208

Last Updated on STN: 19910208 Entered Medline: 19901207

AB The mechanisms by which glycogen metabolism, glycolysis and gluconeogenesis are controlled in the liver both by hormones and by the

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concentration of glucose are reviewed. The control of glycogen metabolism occurs by phosphorylation and dephosphorylation of both glycogen phosphorylase and glycogen synthase catalysed by various protein kinases and protein phosphatases. The hormonal effect is to stimulate glycogenolysis by the intermediary of cyclic AMP, which activates directly or indirectly the protein kinases. The glucose effect is to activate the protein phosphatase system; this occurs by the direct binding of glucose to glycogen phosphorylase which is then a better substrate for phosphorylase phosphatase and is inactivated. Since phosphorylase a is a strong inhibitor of synthase phosphatase, its disappearance allows the activation of glycogen synthase and the initiation of glycogen synthesis. When glycogen synthesis is intense, the concentrations of UDPG and of glucose 6-phosphate in the liver decrease, allowing a net glucose uptake by the liver. Glucose uptake is indeed the difference between the activities of glucokinase and glucose 6-phosphatase. Since the Km of the latter enzyme is far above the physiological concentration of its substrate, the decrease in glucose 6-phosphate concentration proportionally reduces its activity. The control of glycolysis and of gluconeogenesis occurs mostly at the level of the interconversion of fructose 6-phosphate and fructose 1,6-bisphosphate under the action of phosphofructokinase 1 and fructose 1,6-bisphosphatase. Fructose 2,6-bisphosphate is a potent stimulator of the first of these two enzymes and an inhibitor of the second. It is formed from fructose 6-phosphate and ATP by phosphofructokinase 2 and hydrolysed by a fructose 2,6-bisphosphatase. These two enzymes are part of a single bifunctional protein which is a substrate for cyclic AMP-dependent protein kinase. Its phosphorylation causes the inactivation of phosphofructokinase 2 and the activation of fructose 2,6-bisphosphatase, resulting in the disappearance of fructose 2,6-bisphosphate. The other major effector of these two enzymes is fructose 6-phosphate, which is the substrate of phosphofructokinase 2 and a potent **inhibitor** of fructose 2,6-bisphosphatase; these properties allow the formation of fructose 2,6-bisphosphate when the level of glycaemia and secondarily that of fructose 6-phosphate is high.

L74 ANSWER 22 OF 31 MEDLINE DUPLICATE 14

ACCESSION NUMBER: 87305105 MEDLINE

DOCUMENT NUMBER: 87305105 PubMed ID: 3040488

TITLE: Effect of ligands on Drosophila phosphorylase

a as monitored by its enzymic inactivation.

AUTHOR: Dombradi V; Friedrich P; Bot G

SOURCE: INTERNATIONAL JOURNAL OF BIOCHEMISTRY, (1987) 19 (7) 657-9.

Journal code: 0250365. ISSN: 0020-711X.

PUB. COUNTRY: ENGLAND: United Kingdom

DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

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FILE SEGMENT: Priority Journals

ENTRY MONTH: 198710

ENTRY DATE: Entered STN: 19900305

Last Updated on STN: 19980206 Entered Medline: 19871019

AB The dephosphorylation of Drosophila **phosphorylase a** with the catalytic subunit of fruit-fly **protein**

phosphatase-1 was inhibited by AMP, IMP, ADP, ATP, glucose

-6-P, glucose-1-P and UDPG. Glucose, caffeine and

glycogen did not influence the reaction. The inhibitory effect of AMP was reduced by **glucose** and caffeine. The above ligands acted through

the modification of phosphorylase a conformation. This

conclusion was drawn from the ligands' effect on the dephosphorylation of phosphohistone by Drosophila phosphatase-1 and on the tryptic digestion of fruit-fly phosphorylase a.

L74 ANSWER 23 OF 31 MEDLINE

ACCESSION NUMBER: 87109157 MEDLINE

DOCUMENT NUMBER: 87109157 PubMed ID: 2879834

TITLE: Phosphorylation state of acetyl-coenzyme A carboxylase. II.

Variation with nutritional condition.

AUTHOR: Jamil H; Madsen N B

SOURCE: JOURNAL OF BIOLOGICAL CHEMISTRY, (1987 Jan 15) 262 (2)

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Journal code: 2985121R. ISSN: 0021-9258.

PUB. COUNTRY: United States

DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

ENTRY MONTH: 198702

ENTRY DATE: Entered STN: 19900303

Last Updated on STN: 19950206 Entered Medline: 19870225

Acetyl-CoA carboxylase from liver exhibits a linear inverse relationship AR between the ratio of enzymic activities at 0 and 2 mM citrate and the extent of phosphorylation by its kinase, and this citrate activity ratio method was used to examine the effect of nutritional conditions on the phosphorylation state of the enzyme. This method showed that the calculated phosphorylation state, being the extent of phosphorylation at sites accessible to carboxylase kinase, was highest in the livers of starved rats, lower in those fed normally, and lower still in starved rats which had been refed for 48 h on a fat-free diet. The actual values were 0.44, 0.26, and 0 mol of P/subunit, respectively, provided that liver samples were frozen rapidly to liquid nitrogen temperatures and extracted with stopping buffers at temperatures well below freezing. Normal homogenization with stopping buffers (containing inhibitors for protein kinases and phosphatases) resulted in much higher calculated phosphorylation states. The effect of nutritional conditions on the phosphorylation state as estimated reported above was confirmed by purifying the carboxylase from livers of rats, measuring the amount of phosphate which could be incorporated by carboxylase kinase, and comparing this with the phosphorylation state calculated from the citrate activity ratio method or the specific activity. Furthermore, treatment with protein phosphatase of carboxylase from starved rats resulted in the largest increase in specific activity, that from the starved/refed rats in the least. Finally, the effects of hyperglycemia on carboxylase and phosphorylase characteristics in the livers of intact rats were ascertained by taking liver samples and preparing crude extracts by the rapid freezing method described above. Hyperglycemia caused a rapid increase in the activity of the carboxylase and a rapid decrease in its putative phosphorylation state as measured by the citrate activity ratio method. Phosphorylase was also dephosphorylated, as indicated by a decrease in phosphorylase a activity. We conclude that the citrate activity ratio method is a valid test for the phosphorylation state of acetyl-CoA carboxylase in crude extracts of tissue.

L74 ANSWER 24 OF 31 MEDLINE DUPLICATE 15

ACCESSION NUMBER: 87003478

MEDLINE DOCUMENT NUMBER: 87003478 PubMed ID: 3093145

TITLE: Structural and functional properties of Drosophila

melanogaster phosphorylase: comparison with the rabbit

skeletal muscle enzyme.

AUTHOR: Dombradi V; Matko J; Kiss Z; Kiss L; Friedrich P; Bot G SOURCE:

COMPARATIVE BIOCHEMISTRY AND PHYSIOLOGY. B: COMPARATIVE

BIOCHEMISTRY, (1986) 84 (4) 537-43. Journal code: 2984730R. ISSN: 0305-0491.

PUB. COUNTRY: ENGLAND: United Kingdom

DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

ENTRY MONTH: 198611

ENTRY DATE: Entered STN: 19900302

> Last Updated on STN: 19980206 Entered Medline: 19861117

AR Glycogen phosphorylase isolated from Drosophila melanogaster contains one pyridoxal 5'-phosphate per subunit; the coenzyme is in a hydrophobic environment. Fruit-fly **phosphorylase a** has lower KM for glucose-1-phosphate and is less sensitive to allosteric inhibitors than the b form of the enzyme. The amino acid composition of Drosophila phosphorylase differs from that of rabbit skeletal muscle phosphorylase. These two enzymes give distinct one dimensional peptide maps. The distribution of reactive SH-groups is markedly different in the insect and vertebrate phosphorylase. Fruit-fly phosphorylase a is dephosphorylated by either rabbit or Drosophila protein phosphatase-1 at a slower rate than

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rabbit muscle phosphorylase a. MEDLINE DUPLICATE 16 L74 ANSWER 25 OF 31 ACCESSION NUMBER: 85097826 MEDLINE DOCUMENT NUMBER: 85097826 PubMed ID: 2981554 Effects of acidic and basic macromolecules on the activity TITLE: of protein phosphatase-1. AUTHOR: Erdodi F; Csortos C; Bot G; Gergely P SOURCE: BIOCHIMICA ET BIOPHYSICA ACTA, (1985 Jan 21) 827 (1) 23-9. Journal code: 0217513. ISSN: 0006-3002. Netherlands PUB. COUNTRY: DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE) English LANGUAGE: FILE SEGMENT: Priority Journals ENTRY MONTH: 198503 ENTRY DATE: Entered STN: 19900320 Last Updated on STN: 19900320 Entered Medline: 19850320 AB The dephosphorylation of phosphorylase a by the catalytic subunit of protein phosphatase-1 obtained from rabbit skeletal muscle is inhibited by heparin in a noncompetitive manner with respect to phosphorylase a (Ki = 8 micrograms/ml). The inhibitory effect of heparin is also observed in the presence of effectors (e.g., ${\tt glucose}$ and AMP) modifying the dephosphorylation of phosphorylase a. Heat-stable protein inhibitors of protein phosphatase-1 can develop their inhibitory effect of the activity of protein phosphatase-1 even in the presence of heparin. The inhibitory effect of heparin and the heat-stable inhibitor-2 of phosphatase is additive. Polybrene, a heparin antagonist, prevented phosphatase-1 from the inhibition caused by heparin or the inhibitors. Proteins with basic character, histone fractions (H1, H3) and protamine sulfate, can counteract with the inhibitory effect of heparin, but they cannot intercept the actions of inhibitor-1 or -2. L74 ANSWER 26 OF 31 MEDLINE DUPLICATE 17 ACCESSION NUMBER: 84182583 MEDLINE DOCUMENT NUMBER: 84182583 PubMed ID: 6325187 TITLE: Purification and characterization of a protein phosphatase from rat liver acting on key enzymes of glucose metabolism. AUTHOR: Mieskes G; Brand I A; Soling H D SOURCE: EUROPEAN JOURNAL OF BIOCHEMISTRY, (1984 Apr 16) 140 (2) 375-83. Journal code: 0107600. ISSN: 0014-2956. PUB. COUNTRY: GERMANY, WEST: Germany, Federal Republic of DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE) LANGUAGE: English FILE SEGMENT: Priority Journals ENTRY MONTH: 198406 ENTRY DATE: Entered STN: 19900319 Last Updated on STN: 19900319 Entered Medline: 19840607 AB A phosphoprotein phosphatase has been purified from rat liver cytosol. The purification involved chromatography on DEAE-cellulose. Sephacryl S-200, fast protein liquid chromatography (FPLC) and sucrose density gradient centrifugation. It resulted in an almost homogeneous enzyme with a relative molecular mass, Mr, of 90 000 by gel filtration and sucrose gradient centrifugation and Mr = 44 500 by sodium dodecyl sulfate/polyacrylamide gel electrophoresis (SDS-PAGE). Therefore it seems to be a dimeric enzyme. This protein phosphatase (termed PFK-phosphatase) is completely dependent on Mg2+, which can be replaced partly by Mn2+. It can be eluted from DEAE-cellulose with 120 mM NaCl, is not affected by Ca2+, 100 microM trifluoperazine or the heat-stable inhibitor-2. Inhibition occurs with phosphate,

ammonium sulfate and fluoride. PFK-phosphatase dephosphorylates preferentially the alpha subunit of phosphorylase kinase (alpha/beta

histone and casein do not serve as substrates. The enzyme dephosphorylates

dephosphorylation ratio 5-10). Phosphorylase a, mixed

effectively the key enzymes of glucose metabolism

*.	

6-phosphofructo-1-kinase, fructose 1,6-bisphosphatase, pyruvate kinase and 6-phosphofructo-2-kinase. Using this **protein phosphatase** and the catalytic subunit of cAMP-dependent protein kinase, a complete phosphorylation, dephosphorylation and rephosphorylation cycle was possible with 6-phosphofructo-1-kinase as substrate.

L74 ANSWER 27 OF 31 MEDLINE DUPLICATE 18

ACCESSION NUMBER: 83256585 MEDLINE

DOCUMENT NUMBER: 83256585 PubMed ID: 6347198

TITLE: Heterotropic interactions of AMP and glucose

binding sites in phosphorylase a
are destroyed by limited proteolysis.

AUTHOR: Gergely P; Toth B; Dombradi V; Matko J; Bot G

SOURCE: BIOCHEMICAL AND BIOPHYSICAL RESEARCH COMMUNICATIONS, (1983

Jun 29) 113 (3) 825-31.

Journal code: 0372516. ISSN: 0006-291X.

PUB. COUNTRY: United States

DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

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FILE SEGMENT: Priority Journals

ENTRY MONTH: 198308

ENTRY DATE: Entered STN: 19900319

Last Updated on STN: 19980206

Entered Medline: 19830811

AB Subtilisin BPN' hydrolyses a single peptide bond in phosphorylase

a. The two proteolytic fragments are attached to each other by noncovalent bonds in solution as shown by gel filtration and ultracentrifugation studies. The subtilisin nicked phosphorylase

a is inactive, however, still binds AMP and glucose as judged by equilibrium dialysis and fluorescence experiments. The modified enzyme can be dephosphorylated by protein phosphatase and AMP is an effective inhibitor of the dephosphorylation reaction. Glucose cannot cancel the AMP inhibition as well as cannot expel AMP from the nucleotide binding site. Thus a single nick in the polypeptide chain breaks the "communication" between the two ligand binding domains.

L74 ANSWER 28 OF 31 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.

ACCESSION NUMBER: 1982:266404 BIOSIS

DOCUMENT NUMBER: BA74:38884

TITLE: A COMPARISON OF DEPHOSPHORYLATION OF PIG GLYCOGEN

PHOSPHORYLASE A EC-2.4.1.1 ISO ENZYMES.

AUTHOR(S): IMAZU M; KIMURA J; IMAOKA T; USUI H; KINOHARA N; TAKEDA M CORPORATE SOURCE: DEP. OF BIOCHEMISTRY, HIROSHIMA UNIV. SCH. OF MED., KASUMI,

MINAMI-KU, HIROSHIMA 734.

SOURCE: J BIOCHEM (TOKYO), (1982) 91 (1), 49-58.

CODEN: JOBIAO. ISSN: 0021-924X.

FILE SEGMENT: BA; OLD LANGUAGE: English

Muscle, heart (brain) and liver type isoenzymes of glycogen phosphorylase .alpha. were purifed to homogeneity from the pig skeletal muscle, heart and liver. Dephosphorylations of these isoenzymes by phosphoprotein phosphatases [EC 3.1.3.16] with a MW of 224,000 purified from these pig tissues were studied. Apparent Km values of phosphoprotein phosphatases from the skeletal muscle, heart, and liver for the homologous tissue type isoenzymes were 8.8, 9.0, and 8.8 .mu.M, respectively. Apparent Vmax values of dephosphorylation were 2.5, 6.5, and 1.2 nmol/min per unit, respectively (the unit was defined with rabbit skeletal muscle phosphorylase a as a substrate). Inhibition of dephosphorylation of the heart type isoenzyme by G-6-P was partially competitive with a Ki value of 0.05 mM. Though dephosphorylation of the liver type isoenzyme was inhibited competitively by G-6-P with a Ki value of 3.5 mM, dephosphorylation of the muscle type isoenzyme was not affected by 0.1-1 mM G-6-P. AMP was a strong competitive inhibitor of the dephosphorylation reactions with respect to substrate isoenzymes and also served as an allosteric effectors of the heart type isoenzyme. AMP concentrations required for 50% inhibition were 2 .mu.M with the muscle type isoenzyme, 1 .mu.M with the heart type isoenzyme, and 38 .mu.M with the liver type isoenzyme. Differences in Vmax values and in degrees of inhibition by the metabolites of dephosphorylation of the isoenzymes were

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observed with phosphoprotein phosphatases from either homologous or heterologous tissues indicating that these differences were mainly attributed to phosphorylase a isoenzymes. A method for the purification of phosphorylase b from pig liver containing a low level of glycogen was developed.

L74 ANSWER 29 OF 31 CAPLUS COPYRIGHT 2003 ACS

ACCESSION NUMBER: 1981:185841 CAPLUS

DOCUMENT NUMBER: 94:185841

TITLE: Regulation of glycogen phosphorylase and glycogen

synthase by adrenaline in soleus muscle of

DUPLICATE 19

phosphorylase kinase deficient mice

AUTHOR(S): Cohen, Patricia T. W.; Brustel, Yannick Le Marchand;

Cohen, Philip

Dep. Biochem., Univ. Dundee, Dundee, DD1 4HN, UK CORPORATE SOURCE:

European Journal of Biochemistry (1981), 115(3), SOURCE:

619 - 25

CODEN: EJBCAI; ISSN: 0014-2956 Journal

DOCUMENT TYPE:

LANGUAGE: English

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When isolated soleus muscles were incubated with adrenaline (I) [51-43-4], the level of **phosphorylase a** [9032-10-4] in ICR/IAn mice rose from 2.8% in the absence to 5.7% in the presence of I. In contrast, the level of phosphorylase a in normal mice was 2.4-11.1% in the absence of I, and increased to 17.7-23.9%in the presence of the hormone. The trace phosphorylase kinase [9001-88-1] activity in ICR/Ian mice is apparently capable of phosphorylating phosphorylase b in vivo and this enzyme is responsible for the very low level of phosphorylase a in resting soleus muscle of ICR/IAn mice, and perhaps even in normal mice. Since the residual enzyme cannot be activated by cyclic AMP-dependent protein kinase, the elevation of phosphorylase a by I may be caused by an inhibition of phosphorylase phosphatase. The possibility that this occurs through the activation of protein phosphatase inhibitor 1 by cyclic AMP-dependent protein kinase is discussed. Incubation of soleus muscles with I decreased the activity ratio (.+-.glucose 6-phosphate) of glycogen synthase (EC 2.4.1.11) [9014-56-6] from 0.24 to 0.08 in ICR/IAn mice and from 0.31 to 0.14 in C3H/He-mg or Swiss albino mice. Thus, the inactivation of glycogen synthase by I in resting soleus muscle does not result from the activation of phosphorylase kinase by cyclic AMP-dependent protein kinase. It is most likely mediated by a direct phosphorylation catalyzed by cyclic AMP-dependent protein kinase, although the activation of protein phosphatase inhibitor 1 may also contribute to the effect.

L74 ANSWER 30 OF 31 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.

ACCESSION NUMBER:

1983:215894 BIOSIS

DOCUMENT NUMBER:

BA75:65894

TITLE:

REGULATION BY PHOSPHORYLASE KINASE OF PHOSPHO PROTEIN PHOSPHATASE ACTIVITY SIMULTANEOUS

CONTROL OF PROTEIN PHOSPHORYLATION AND DEPHOSPHORYLATION IN

SKELETAL MUSCLE.

AUTHOR(S):

GERGELY P; BOT G

CORPORATE SOURCE:

INST. OF MED. CHEM., H-4012 DEBRECEN, BEM-TER, 18/B,

HUNGARY.

SOURCE:

ACTA BIOCHIM BIOPHYS ACAD SCI HUNG, (1981 (RECD 1982)) 16

(3-4), 163-178.

CODEN: ABBPAP. ISSN: 0001-5253.

FILE SEGMENT: BA; OLD LANGUAGE: English

٠.

Phosphorylase kinase from rabbit skeletal muscle inhibited the dephosphorylation of phosphorylase a by phosphorprotein phosphatase. Phosphorylation (activation) of phosphorylase kinase by cAMP-dependent protein kinase greatly increased this inhibitory effect. Phosphoprotein phosphatase in inhibited by phosphorylase kinase in a reversible manner. The regulation by phosphorylase kinase at phosphoprotein phosphatase activity in different fractions of muscle extract and in the presence of various ligands was investigated. The presence of phosphorylase kinase also affected the ligand control of phosphatase activity. Phosphorylase kinase almost cancelled the inhibitory effect of AMP but hardly influenced the activating effect of glucose, G-6-P and caffeine. Calmodulin, glycogen and phosphorylase b (effectors of phosphorylase kinase) did not influence the inhibitory effect of phosphorylase kinase. Fractions of muscle extract also demonstrated the regulatory role of phosphorylase kinase. These fractions contained considerable amounts of phosphorylase kinase and phosphatase. Phosphatase activity was inhibited by phosphorylation reactions triggered by Mg2+ and ATP. Heat-stable inhibitors were absent from these fractions; therefore the transient inhibition of phosphatase could be attributed to the phosphorylation of endogenous phosphorylase kinase. The introduction between phosphorylase kinase and phosphatase resulted in a loss of AMP sensitivity, i.e., AMP did not inhibit the activity of phosphatase in those fractions. The phosphorylation of phosphorylase kinase is equally important both in the formation of enzymatically active phsophorylase a and in the inhibition of

L74 ANSWER 31 OF 31 CAPLUS COPYRIGHT 2003 ACS ACCESSION NUMBER: 1978:575597 CAPLUS

DOCUMENT NUMBER:

89:175597

TITLE: The substrate specificity and regulation of the

protein phosphatases involved in the

control of glycogen metabolism in mammalian skeletal

muscle

AUTHOR(S): Cohen, Philip; Nimmo, Gillian A.; Burchell, Ann;

Antoniw, John F.

dephosphorylation of phosphorylase a. The consequence of these 2 effects is the elevated level of phosphorylase

CORPORATE SOURCE: Dep. Biochem., Univ. Dundee, Dundee, UK

SOURCE: Advances in Enzyme Regulation (1978), 16, 97-119

CODEN: AEZRA2; ISSN: 0065-2571

DOCUMENT TYPE: Journal LANGUAGE: English

Protein phosphatase-III, which catalyzes the

dephosphorylation of the .beta.-subunit of phosphorylase kinase, phosphorylase a, and glycogen synthetase bl and b2 (

glucose 6-phosphate-dependent forms produced by cyclic

AMP-dependent protein kinase and glycogen synthetase kinase-2, resp.), was purified 2500-fold from muscle. The mol. wt. was .apprx.130,000-140,000 and on Na dodecyl sulfate-polyacrylamide gel electrophoresis, one band of mol. wt. 35,000 was obsd., suggesting that the enzyme is a tetramer.

Protein phosphatase-II, which dephosphorylates phosphorylase kinase .alpha.-subunit, was also purified 2500-fold from muscle and its specificity compared to that of phosphatase-III. The different substrate specificities, mol. wts., and response to inhibitor-2 (a heat-stable protein from muscle specific for phosphatase-III) suggests that they are distinct proteins. Inhibitor-1, which only inhibits phosphatass-III after being phosphorylated by cyclic AMP-dependent protein kinase, was purified 4000-fold to homogeneity from skeletal muscle. The amino acid compn. showed the complete absence of cysteine, tyrosine, and tryptophan, a very low hydrophobic amino acid content, and a high content of glutamic acid and proline. The mol. wt. was .apprx.20,000. The possible physiol. roles of inhibitor-1 and inhibitor-2 are discussed.

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WEST Search History

DATE: Monday, January 13, 2003

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DB=USP7	T,PGPB,JPAB,EPAB,DWPI; THES=ASSIGNEE; PLUR=YES; OP=ADJ		
L7	L6 and 15	46	L7
L6	L2 and (inhibitor or modulator or agonist or antagonist)	1339	L6
L5	L4 and (glycogen synthase or glycogen synthetase)	66	L5
L4	L2 and (diabetes or glucose)	987	L4
L3	L2 and glycogen targeting	1	L3
L2	phosphorylase and phosphatase	1697	L2
L1	phosphorylase a and protein phosphatase	0	L1

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Search Results - Record(s) 1 through 1 of 1 returned.

1. Document ID: JP 2002532381 W WO 200012549 A1 AU 9954368 A EP 1107986 A1

L3: Entry 1 of 1

File: DWPI

Oct 2, 2002

DERWENT-ACC-NO: 2000-256587

DERWENT-WEEK: 200279

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TITLE: Lowering blood sugar levels in the treatment of diabetes, using a compound that blocks interaction between phosphorylase alpha and protein phosphatase I glycogen-targeting subunit

INVENTOR: ARMSTRONG, C G; COHEN, P T W; DOHERTY, M J

PRIORITY-DATA: 1998GB-0018650 (August 27, 1998)

PATENT-FAMILY:

PUB-NO	PUB-DATE	LANGUAGE	PAGES	MAIN-IPC
JP 2002532381 W	October 2, 2002		041	A61K045/00
WO 200012549 A1	March 9, 2000	E	026	C07K014/47
AU 9954368 A	March 21, 2000		000	C07K014/47
EP 1107986 A1	June 20, 2001	E	000	C07K014/47

ABSTRACTED-PUB-NO: WO 200012549A

BASIC-ABSTRACT:

NOVELTY - The medicinal use of a compound (C1) capable of blocking the interaction of phosphorylase alpha with the glycogen-targeting subunit (GL) of protein phosphatase I, is new.

DETAILED DESCRIPTION - An INDEPENDENT CLAIM is also included for a method (A) for identifying C1.

USE - The invention is used to reduce the blood glucose level of a mammal, particularly a human (claimed), in hyperglycemic disorders such as type I or type II diabetes.

ADVANTAGE - None given

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments	Claims	KVVIC	Drawi Desc	Imag
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Search Results - Record(s) 1 through 20 of 46 returned.

1. Document ID: US 20030004162 A1

L7: Entry 1 of 46 File: PGPB Jan 2, 2003

PGPUB-DOCUMENT-NUMBER: 20030004162

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20030004162 A1

TITLE: Use of glycogen phosphorylase inhibitors

PUBLICATION-DATE: January 2, 2003

INVENTOR-INFORMATION:

NAME CITY STATE COUNTRY RULE-47

Treadway, Judith L. Mystic CT US

US-CL-CURRENT: 514/228.2; 514/233.5, 514/254.09, 514/365, 514/415

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments	Claims	KMC	Drawi Desc	Image

2. Document ID: US 20020198205 A1

L7: Entry 2 of 46 File: PGPB Dec 26, 2002

PGPUB-DOCUMENT-NUMBER: 20020198205

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20020198205 A1

TITLE: Xanthine derivatives, the preparation thereof and their use as pharmaceutical

compositions

PUBLICATION-DATE: December 26, 2002

INVENTOR - INFORMATION:

NAME CITY STATE COUNTRY RULE-47 Mittelbiberach Himmelsbach, Frank DE Mark, Michael Biberach DE Eckhardt, Matthias Biberach DE Langkopf, Elke Warthausen DE Maier, Roland Biberach DE Lotz, Ralf Schemmerhofen DE

US-CL-CURRENT: 514/234.5; 514/252.16, 514/263.2, 514/263.22, 514/263.35, 544/118, 544/272, 544/276

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments	Claims	KWIC	Draw Desc	Image
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3. Document ID: US 20020198158 A1

L7: Entry 3 of 46 File: PGPB Dec 26, 2002

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PGPUB-DOCUMENT-NUMBER: 20020198158

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20020198158 A1

TITLE: Use of a cyclic ether for the preparation of medicaments affecting glucose tolerance

PUBLICATION-DATE: December 26, 2002

INVENTOR - INFORMATION:

NAME

CITY

STATE

COUNTRY

RULE-47

Ahren, Bo

Lund

Yu, Shukun

Malmoe

SE

US-CL-CURRENT: <u>514/23</u>; <u>514/460</u>, <u>514/473</u>

 r Front Review	Classification Da	te Mererense	Sequences	Attachments	Clambi V	WMC Draw, Desc	Image

4. Document ID: US 20020151463 A1

L7: Entry 4 of 46

File: PGPB

Oct 17, 2002

PGPUB-DOCUMENT-NUMBER: 20020151463

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20020151463 A1

TITLE: Agouti polynucleotide compositions and methods of use

PUBLICATION-DATE: October 17, 2002

INVENTOR - INFORMATION:

CITY

STATE

RULE-47

Woychik, Richard P.

Orinda

CA OH US

COUNTRY

Bultman, Scott J. Michaud, Edward J. Lakewood

US

US

US-CL-CURRENT: 514/2; 435/325, 435/6, 435/69.1, 536/23.5

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments	KWWC Draws Des	: Image

5. Document ID: US 20020142981 A1

L7: Entry 5 of 46

File: PGPB

Oct 3, 2002

PGPUB-DOCUMENT-NUMBER: 20020142981

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20020142981 A1

TITLE: Gene expression profiles in liver cancer

PUBLICATION-DATE: October 3, 2002

INVENTOR-INFORMATION:

NAME CITY

Gaithersburg

STATE COUNTRY MD US

RULE-47

Horne, Darci T. Scherf, Uwe

Gaithersburg

MD

US

Vockley, Joseph

Damascus

MD

US

US-CL-CURRENT: 514/44; 435/6

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Full Title Citation Front Review Classification Date Reference Sequences Attachments KWC Draw Desc Image 6. Document ID: US 20020077466 A1 L7: Entry 6 of 46 File: PGPB Jun 20, 2002

PGPUB-DOCUMENT-NUMBER: 20020077466

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20020077466 A1

TITLE: Polypeptides and nucleic acids encoding same

PUBLICATION-DATE: June 20, 2002

INVENTOR-INFORMATION:

NAME CITY STATE COUNTRY RULE-47 Spaderna, Steven K. Berlin CT US CTUS Quinn, Kerry E. Hamden West Haven CTUS Shimkets, Richard A. Branford CTUS Padigaru, Muralidhara Spytek, Kimberly A. New Haven CTUS

US-CL-CURRENT: 536/23.5; 424/130.1, 435/320.1, 435/325, 435/6, 435/7.1, 530/324, 530/387.9, <u>800/3</u>

Full	Title	Citation Front	Review Classification	Date Reference	Sequences	Affachments	Kowic	Draw, Desc	Image
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	7.	Document ID:	US 2002007673	9 A1					

File: PGPB

PGPUB-DOCUMENT-NUMBER: 20020076739

PGPUB-FILING-TYPE: new

L7: Entry 7 of 46

DOCUMENT-IDENTIFIER: US 20020076739 A1

TITLE: Rapid quantitative analysis of proteins or protein function in complex mixtures

PUBLICATION-DATE: June 20, 2002

INVENTOR-INFORMATION:

NAME CITY STATE COUNTRY RULE-47 Aebersold, Rudolf Hans Mercer Island WA US Gelb, Michael H. Seattle WA US Gygi, Steven P. Seattle WA US Scott, C. Ronald WA US Seattle Turecek, Frantisek Seattle WA US Gerber, Scott A. Seattle WA US Rist, Beate Seattle WA US

US-CL-CURRENT: 435/7.92; 530/403

	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments	KWMC Draw, Desc Imag
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L7: Entry 8 of 46 File: PGPB May 30, 2002

Jun 20, 2002

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PGPUB-DOCUMENT-NUMBER: 20020065221

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20020065221 A1

TITLE: Control of protein synthesis, and screening method for agents

PUBLICATION-DATE: May 30, 2002

INVENTOR-INFORMATION:

CITY STATE COUNTRY RULE-47 NAME

Cohen, Philip Dundee GB Alessi, Dario Dundee GB Cross, Darren Dundee GB

US-CL-CURRENT: 514/12; 424/94.5

Full	Title	Citation	Front	Review	Classification			Attachments	KMC Draw Desc Image
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L7: Entry 9 of 46

File: PGPB

Mar 14, 2002

PGPUB-DOCUMENT-NUMBER: 20020032323

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20020032323 A1

TITLE: STREPTOCOCCUS PNEUMONIAE POLYNUCLEOTIDES AND SEQUENCES

PUBLICATION-DATE: March 14, 2002

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
KUNSCH, CHARLES A.	GAITHERSBURG	MD	US	
CHOI, GIL H.	ROCKVILLE	MD	US	
DILLON, PATRICK J.	CARLSBAD	CA	US	
ROSEN, CRAIG A.	LAYTONSVILLE	MD	US	
BARASH, STEVEN C.	ROCKVILLE	MD	US	
FANNON, MICHAEL R.	SILVER SPRING	MD	US	
DOUGHERTY, BRIAN A.	MT. AIRY	MD	US	

US-CL-CURRENT: <u>536/23.7</u>; <u>435/252.3</u>, <u>435/320.1</u>, <u>435/69.1</u>, <u>536/24.32</u>

Full	Title Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments	KWIC	Drawt Desig	Imag

L7: Entry 10 of 46 File: PGPB Mar 7, 2002

PGPUB-DOCUMENT-NUMBER: 20020028477

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20020028477 A1

TITLE: Assay for kinases and phosphatases

PUBLICATION-DATE: March 7, 2002

INVENTOR - INFORMATION:

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NAME CITY STATE COUNTRY WI US Fitchburg Goueli, Said Vidugiriene, Jolanta Madison WI US US Karassina, Natasha Madison WΤ

US-CL-CURRENT: 435/15

Full Title Citation Front Review Classification Date Reference Sequences Attachments

KWIC Draw. Desc Image

RULE-47

11. Document ID: US 20020026111 A1

L7: Entry 11 of 46

File: PGPB

Feb 28, 2002

PGPUB-DOCUMENT-NUMBER: 20020026111

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20020026111 A1

TITLE: Methods of monitoring glucose levels in a subject and uses thereof

PUBLICATION-DATE: February 28, 2002

INVENTOR-INFORMATION:

NAME CITY STATE COUNTRY RULE-47

Ackerman, Neil San Carlos CA US

US-CL-CURRENT: 600/347; 128/921, 600/300

Full Title Citation Front Review Classification Date Reference Sequences Attachments KMC Draw. Desc Image

12. Document ID: US 6503729 B1

L7: Entry 12 of 46 File: USPT Jan 7, 2003

US-PAT-NO: 6503729

DOCUMENT-IDENTIFIER: US 6503729 B1

TITLE: Selected polynucleotide and polypeptide sequences of the methanogenic archaeon,

methanococcus jannashii

DATE-ISSUED: January 7, 2003

INVENTOR-INFORMATION:

NAME CITY STATE ZIP CODE COUNTRY

Bult; Carol J.

Bar Harbor

ME

White; Owen R.

Gaithersburg

MD

Smith; Hamilton O.

Baltimore

MD

Woese; Carl R.

Urbana

IL

Venter; J. Craiq

Rockville

MD

US-CL-CURRENT: 435/69.1; 435/252.3, 435/320.1, 435/325, 536/23.1, 536/23.5

ABSTRACT:

The present application describes selected polynucleotide sequence from the 1.66-megabase pair genome sequence of an autotrophic archaeon, Methanococcus jannaschii, and its 58- and 16-kilobase pair extrachromosomal elements.

107 Claims, 2 Drawing figures Exemplary Claim Number: 1 Number of Drawing Sheets: 2

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Full Title Citation Front Review Classification Date Reference Sequences Attachments KWC Draw Desc Image

13. Document ID: US 6479055 B1

L7: Entry 13 of 46 File: USPT Nov 12, 2002

US-PAT-NO: 6479055

DOCUMENT-IDENTIFIER: US 6479055 B1

TITLE: Methods for inhibition of membrane fusion-associated events, including respiratory

syncytial virus transmission

DATE-ISSUED: November 12, 2002

INVENTOR-INFORMATION:

NAME CITY STATE ZIP CODE COUNTRY Bolognesi; Dani Paul Durham NC Durham NC Matthews; Thomas James NC Durham Wild; Carl T. Barney; Shawn O'Lin NC Cary Lambert; Dennis Michael NC Cary NC Petteway; Stephen Robert Cary Durham NC Langlois; Alphonse J.

US-CL-CURRENT: 424/211.1; 424/186.1, 530/324

ABSTRACT:

The present invention relates to peptides which exhibit potent anti-viral activity. In particular, the invention relates to methods of using such peptides as inhibitory of respiratory syncytial virus ("RSV") transmission to uninfected cells. The peptides used in the methods of the invention are homologs of the DP-178 and DP-107 peptides, peptides corresponding to amino acid residues 638 to 673, and to amino acid residues 558 to 595, respectively, of the HIV-1.sub.LAI transmembrane protein (TM) gp41.

44 Claims, 84 Drawing figures Exemplary Claim Number: 1 Number of Drawing Sheets: 83

Full Title Citation Front Review Classific	ation Date Reference Sequences Attachment	S KWMC Draws Desc Image
14. Document ID: US 644105	53 B1	
L7: Entry 14 of 46	File: USPT	Aug 27, 2002

US-PAT-NO: 6441053

DOCUMENT-IDENTIFIER: US 6441053 B1

TITLE: Inhibitors of glycogen synthase kinase-3 and methods for identifying and using the same

DATE-ISSUED: August 27, 2002

INVENTOR - INFORMATION:

NAME CITY STATE ZIP CODE COUNTRY

Klein; Peter S. Wynnewood PA Melton; Douglas Lexington MA

US-CL-CURRENT: 514/789; 424/610, 435/15, 514/183, 514/211.01, 514/410

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ABSTRACT:

A method of identifying <u>inhibitors of glycogen synthase</u> kinase-3 is provided. The method comprises providing a mixture comprising GSK-3, a phosphate source, and a GSK-3 substrate, incubating the mixture in the presence or absence of a test compound, and assessing the activity of GSK-3 in the mixture. A reduction of GSK-3 activity following incubation of the mixture in the presence of the test compound is an indication that the test compound is an inhibitor of GSK-3.

1 Claims, 20 Drawing figures Exemplary Claim Number: 1 Number of Drawing Sheets: 10

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments	KWIC [)raw. Desc	lmage
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15. Document ID: US 6391595 B1

L7: Entry 15 of 46

File: USPT

May 21, 2002

US-PAT-NO: 6391595

DOCUMENT-IDENTIFIER: US 6391595 B1

TITLE: Transferase and amylase, process for producing the enzymes, use thereof, and gene coding

for the same

DATE-ISSUED: May 21, 2002

INVENTOR - INFORMATION:

NAME CITY STATE ZIP CODE COUNTRY

Kato; Masaru Takasaki JP
Miura; Yutaka Takasaki JP

US-CL-CURRENT: 435/100; 435/183, 435/194, 435/200, 435/91.53, 435/97

ABSTRACT:

The invention provides a novel transferase that acts on a saccharide, as a substrate, composed of at least three sugar units wherein at least three glucose residues on the reducing end are linked .alpha.-1,4 so as to transfer the .alpha.-1,4 lingages to a .alpha.-1,.alpha.-1 linkages; a process for producing the transferase; a gene coding for the same; and a process for producing an oligosaccharide by using the same. Also provided are a novel amylase that has a principal activity of acting on a saccharide, as a substrate, composed of at least three sugar units wherein at least three sugar units on the reducing end side are glucose units and the linkage between the first and the second glucose units is .alpha.-1,.alpha.-1 while the linkage between the second and the third glucose units is .alpha.-1,4 so as to liberate .alpha..alpha.-trehalose by hydrolyzing the .alpha.-1,4 linkage and another activity of hydrolyzing the .alpha.-1,4 linkage within the molecular chain of the substrate and that liberates disaccharides and/or monosaccharides as the principal final products; a process for producing the amylase; a gene coding for the same; and a process for producing .alpha.-trehalose by using a combination of the transferase and the amylase.

38 Claims, 51 Drawing figures Exemplary Claim Number: 1 Number of Drawing Sheets: 44

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments	KWWC Drawn Desc
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16. Document ID: US 6335170 B1

L7: Entry 16 of 46 File: USPT Jan 1, 2002

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US-PAT-NO: 6335170

DOCUMENT-IDENTIFIER: US 6335170 B1

TITLE: Gene expression in bladder tumors

DATE-ISSUED: January 1, 2002

INVENTOR-INFORMATION:

NAME CITY STATE ZIP CODE COUNTRY

Orntoft; Torben F. DK 8230 Aabyhoj DK

US-CL-CURRENT: 435/6; 435/91.1, 435/91.2, 536/23.1, 536/24.3, 536/24.31, 536/24.33

ABSTRACT:

Methods for analyzing tumor cells, particularly bladder tumor cells employ gene expression analysis of samples. Gene expression patterns are formed and compared to reference patterns. Alternatively gene expression patterns are manipulated to exclude genes which are expressed in contaminating cell populations. Another alternative employs subtraction of the expression of genes which are expressed in contaminating cell types. These methods provide improved accuracy as well as alternative basis for analysis from diagnostic and prognostic tools currently available.

21 Claims, 24 Drawing figures Exemplary Claim Number: 1 Number of Drawing Sheets: 15

Full T	itle Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments	ł	OMC C	raw. De:	sc	Image
	17. Docui	ment II): US	6331396 B	l						***************************************	***********	***************************************
L7: Ent	try 17 of	46				File	e: USPT			Dec	: 18,	200	1

US-PAT-NO: 6331396

DOCUMENT-IDENTIFIER: US 6331396 B1

TITLE: Arrays for identifying agents which mimic or inhibit the activity of interferons

DATE-ISSUED: December 18, 2001

INVENTOR-INFORMATION:

NAME CITY STATE ZIP CODE COUNTRY Silverman; Robert H. Beachwood OH Williams; Bryan R. G. Cleveland OH Cleveland OH

US-CL-CURRENT: 435/6; 435/287.2, 536/23.1, 536/23.52, 536/24.3, 536/24.31

ABSTRACT:

Methods and model systems for identifying and characterizing new therapeutic agents, particularly proteins, which mimic or inhibit the activity of all interferons, Type I interferons, IFN-.alpha., IFN-.beta., or IFN-.gamma. The method comprises administering an interferon selected from the group consisting of IFN-.alpha., IFN .beta., IFN-.tau., IFN-.omega., IFN-.gamma., and combinations thereof to cultured cells, administering the candidate agent to a duplicate culture of cells; and measuring the effect of the candidate agent and the interferon on the transcription or translation of one or, preferably, a plurality of the interferon stimulated genes or the interferon repressed genes (hereinafter referred to as "ISG's" and "IRGs", respectively). The model system is an array with gene probes that hybridize with from about 100 to about 5000 ISG and IRG transcripts.

8 Claims, 0 Drawing figures Exemplary Claim Number: 1

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18. Document ID: US 6326141 B1

L7: Entry 18 of 46

File: USPT

Dec 4, 2001

US-PAT-NO: 6326141

DOCUMENT-IDENTIFIER: US 6326141 B1

TITLE: Methods for determining risk for Type I and Type II diabetes

DATE-ISSUED: December 4, 2001

INVENTOR - INFORMATION:

NAME

CITY

STATE

ZIP CODE

COUNTRY

Kahn; C. Ronald
Reynet; Christine

West Newton Boston MA MA

US-CL-CURRENT: 435/6; 435/7.1, 536/23.2, 536/23.5

ABSTRACT:

Purified DNA including a sequence encoding Diabetogene rad.

14 Claims, 3 Drawing figures Exemplary Claim Number: 1 Number of Drawing Sheets: 5

Ful	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments	KWIC	Draw, Desc	Image
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19. Document ID: US 6310034 B1

L7: Entry 19 of 46

File: USPT

Oct 30, 2001

COUNTRY

US-PAT-NO: 6310034

DOCUMENT-IDENTIFIER: US 6310034 B1

TITLE: Agouti polypeptide compositions

DATE-ISSUED: October 30, 2001

INVENTOR-INFORMATION:

NAME CITY STATE ZIP CODE

Woychik; Richard P. Orinda CA Bultman; Scott J. Lakewood OH

Michaud; Edward J. Kingston TN

US-CL-CURRENT: 514/2; 530/300, 530/350

ABSTRACT:

Disclosed are methods and compositions comprising novel agouti polypeptides and the polynucleotides which encode them. Also disclosed are DNA segments encoding these proteins derived from human and murine cell lines, and the use of these polynucleotides and polypeptides in a variety of diagnostic and therapeutic applications. Methods, compositions, kits, and devices are also provided for identifying compounds which are <u>inhibitors</u> of agouti activity, and for altering fatty acid synthetase activity and intracellular calcium levels in transformed cells.

34 Claims, 83 Drawing figures Exemplary Claim Number: 1

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Number of Drawing Sheets: 41

Full Title Citation Front Review Classification Date Reference Sequences Attachments KMC Draw Desc Image

20. Document ID: US 6297359 B1

L7: Entry 20 of 46 File: USPT Oct 2, 2001

US-PAT-NO: 6297359

DOCUMENT-IDENTIFIER: US 6297359 B1

TITLE: Protein phosphatase 1 binding protein, R5

DATE-ISSUED: October 2, 2001

INVENTOR-INFORMATION:

NAME CITY STATE ZIP CODE COUNTRY

Young; Peter R. Lawrenceville NJ

Cohen; Patricia T. W. Dundee GB
Cohen; Phillip Dundee GB

US-CL-CURRENT: 530/350; 435/183, 435/69.1, 536/23.1

ABSTRACT:

Human PPP1R5 polypeptides and DNA (RNA) encoding such PPP1R5 and a procedure for producing such polypeptides by recombinant techniques is disclosed. Also disclosed are methods for utilizing such PPP1R5, or compounds which inhibit or stimulate PPP1R5 for dysfunctions or diseases which involve resistance to the action of insulin on glycogen synthesis are also disclosed. Agonist and antagonists of these PPP1R5 proteins and methods of their use are also disclosed. Also disclosed are diagnostic assays for detecting diseases related to mutations in the nucleic acid sequences and altered concentrations of the polypeptides. Also disclosed are diagnostic assays for detecting mutations in the polynucleotides encoding the PPP1R5 and for detecting altered levels of the polypeptide in a host.

4 Claims, 5 Drawing figures Exemplary Claim Number: 1 Number of Drawing Sheets: 5

Full Title C	itation Front	Review	Classification	Date	Reference	Sequences	Attachments	KWIC	Drawu Desc
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Search Results - Record(s) 21 through 40 of 46 returned.

21. Document ID: US 6258547 B1

L7: Entry 21 of 46

File: USPT

Jul 10, 2001

US-PAT-NO: 6258547

DOCUMENT-IDENTIFIER: US 6258547 B1

TITLE: Nucleic acid encoding amp-activated protein kinase

DATE-ISSUED: July 10, 2001

INVENTOR - INFORMATION:

NAME CITY STATE ZIP CODE COUNTRY

Beri; Rajinder Kumar Macclesfield GB
Carling; David London GB
Forder; Robert Anthony Macclesfield GB

US-CL-CURRENT: 435/7.1; 435/183, 435/69.1, 530/300, 530/325, 530/350, 530/387.1, 536/23.2,

536/23.4

ABSTRACT:

cDNAs encoding mammalian AMP protein kinases, corresponding polypeptides and recombinant proteins together with antibodies thereto. Their uses including the study of gene expression and the characteristics of other proteins.

20 Claims, 24 Drawing figures Exemplary Claim Number: 1 Number of Drawing Sheets: 20

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments	Claims	KWIC	Drawi Desc	100
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22. Document ID: US 6252057 B1

L7: Entry 22 of 46

File: USPT

Jun 26, 2001

US-PAT-NO: 6252057

DOCUMENT-IDENTIFIER: US 6252057 B1

TITLE: Protein targeting to glycogen

DATE-ISSUED: June 26, 2001

INVENTOR - INFORMATION:

NAME CITY STATE ZIP CODE COUNTRY

Brady; Matthew Jemail Ann Arbor MI
Printen; John Andrew Ann Arbor MI
Saltiel; Alan Robert Ann Arbor MI

US-CL-CURRENT: 536/23.5; 435/320.1, 435/325, 530/350

ABSTRACT:

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The present invention provides human and murine genomic and complementary DNA and the proteins that are encoded by the DNA, which is called "Protein Targeting to Glycogen". Also provided is a method of increasing the amount of glycogen in a cell.

14 Claims, 12 Drawing figures Exemplary Claim Number: 1,2 Number of Drawing Sheets: 9

Full Title Citation Front Review Classification Date Reference Sequences Attachments Claims KMC Draw Desc Image

23. Document ID: US 6228983 B1

L7: Entry 23 of 46

File: USPT

May 8, 2001

US-PAT-NO: 6228983

DOCUMENT-IDENTIFIER: US 6228983 B1

TITLE: Human respiratory syncytial virus peptides with antifusogenic and antiviral activities

DATE-ISSUED: May 8, 2001

INVENTOR-INFORMATION:

NAME CITY STATE ZIP CODE COUNTRY

Barney; Shawn O'Lin Cary NC
Lambert; Dennis Michael Cary NC
Petteway; Stephen Robert Cary NC

US-CL-CURRENT: 530/300; 424/186.1, 424/211.1, 530/324, 530/325, 530/326

ABSTRACT:

The present invention relates to peptides which exhibit antifusogenic and antiviral activities. The peptides of the invention consist of a 16 to 39 amino acid region of a human respiratory syncytial virus protein. These regions were identified through computer algorithms capable of recognizing the ALLMOTI5, 107x178x4, or PLZIP amino acid motifs. These motifs are associated with the antifusogenic and antiviral activities of the claimed peptides.

62 Claims, 84 Drawing figures Exemplary Claim Number: 1 Number of Drawing Sheets: 83

Full	Titte	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments	Claims	KWIC	Draw. Desc	Image

24. Document ID: US 6204248 B1

L7: Entry 24 of 46

File: USPT

Mar 20, 2001

US-PAT-NO: 6204248

DOCUMENT-IDENTIFIER: US 6204248 B1

TITLE: Pharmaceutical preparations of glutathione and methods of administration thereof

DATE-ISSUED: March 20, 2001

INVENTOR-INFORMATION:

NAME CITY STATE ZIP CODE COUNTRY

Demopoulos; Harry B. Scarsdale NY Seligman; Myron L. Fairfield CT

US-CL-CURRENT: 514/21; 514/18

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ABSTRACT:

A method of altering an expression of a gene product in cells or an organism, comprising orally administering glutathione in an effective amount and under such conditions to alter a redox potential in the cells. The gene expression may be sensitive to redox potential through one or more of a process of induction, transcription, translation, post-translational modification, release, and/or through a receptor mediated process. The glutathione is preferably administered as an oral bolus of encapsulated pharmaceutically stabilized glutathione in a rapidly dissolving formulation to a mammal on an empty stomach.

14 Claims, 2 Drawing figures Exemplary Claim Number: 1 Number of Drawing Sheets: 2

Full Title Citation Front Review Classification Date Reference Sequences Attachments

KMC Draw Desc Image

25. Document ID: US 6165500 A

L7: Entry 25 of 46

File: USPT

Dec 26, 2000

US-PAT-NO: 6165500

DOCUMENT-IDENTIFIER: US 6165500 A

TITLE: Preparation for the application of agents in mini-droplets

DATE-ISSUED: December 26, 2000

INVENTOR-INFORMATION:

NAME CITY STATE ZIP CODE COUNTRY

Cevc; Gregor Heimstetten DE

US-CL-CURRENT: 424/450; 424/94.3, 428/402.2

ABSTRACT:

The invention relates to a preparation for the application of agents in the form of minuscule droplets of fluid, in particular provided with membrane-like structures consisting of one or several layers of amphiphilic molecules, or an amphiphilic carrier substance, in particular for transporting the agent into and through natural barriers such as skin and similar materials. The preparation contains a concentration of edge active substances which amounts to up to 99 mol-% of the agent concentration which is required for the induction of droplet solubilization. Such preparations are suitable, for example, for the non-invasive applications of antidiabetics, in particular of insulin. The invention, moreover, relates to the methods for the preparation of such formulations.

35 Claims, 31 Drawing figures Exemplary Claim Number: 1 Number of Drawing Sheets: 21

Full Title Citation Front Review Classification Date Reference Sequences Attachments

KWWC Draw Desc Image

26. Document ID: US 6114304 A

L7: Entry 26 of 46

File: USPT

Sep 5, 2000

US-PAT-NO: 6114304

DOCUMENT-IDENTIFIER: US 6114304 A

TITLE: Methods for regulating gastrointestinal motility

DATE-ISSUED: September 5, 2000

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INVENTOR - INFORMATION:

NAME CITY STATE ZIP CODE COUNTRY

Kolterman; Orville G. Poway CA
Young; Andrew A. Alpine CA
Rink; Timothy J. La Jolla CA
Brown; Kathleen Ann Keiting Wake Forest NC

US-CL-CURRENT: <u>514/12</u>; <u>514/3</u>

ABSTRACT:

Methods for treating conditions associated with elevated, inappropriate or undesired post-prandial blood glucose levels are disclosed which comprise administration of an effective amount of an amylin agonist alone or in conjunction with other anti-gastric emptying agents. Methods for reducing gastric motility and delaying gastric emptying for therapeutic and diagnostic purposes are also described.

35 Claims, 17 Drawing figures Exemplary Claim Number: 1 Number of Drawing Sheets: 17

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	Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments	KWIC	Draw, Desc	Image

27. Document ID: US 6093794 A

L7: Entry 27 of 46 File: USPT Jul 25, 2000

US-PAT-NO: 6093794

DOCUMENT-IDENTIFIER: US 6093794 A

TITLE: Isolated peptides derived from the Epstein-Barr virus containing fusion inhibitory

domains

DATE-ISSUED: July 25, 2000

INVENTOR - INFORMATION:

NAME CITY STATE ZIP CODE COUNTRY

Barney; Shawn O'Lin Cary NC
Lambert; Dennis Michael Cary NC
Petteway; Stephen Robert Cary NC

US-CL-CURRENT: 530/300; 424/186.1, 424/230.1, 530/324, 530/325, 530/326, 530/350

ABSTRACT:

The present invention relates to peptides which exhibit potent

anti-retroviral activity. The peptides of the invention comprise DP178 (SEQ ID:1) peptide corresponding to amino acids 638 to 673 of the HIV-1.sub.LAI gp41 protein, and fragments, analogs and homologs of DP178. The invention further relates to the uses of such peptides as inhibitory of human and non-human retroviral, especially HIV, transmission to uninfected cells.

27 Claims, 52 Drawing figures Exemplary Claim Number: 1 Number of Drawing Sheets: 83

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments	KWMC	Draw, Desc	Image

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28. Document ID: US 6068973 A

L7: Entry 28 of 46 File: USPT May 30, 2000

US-PAT-NO: 6068973

DOCUMENT-IDENTIFIER: US 6068973 A

TITLE: Methods for inhibition of membrane fusion-associated events, including influenza virus

DATE-ISSUED: May 30, 2000

INVENTOR-INFORMATION:

NAME CITY STATE ZIP CODE COUNTRY

Barney; Shawn O'Lin Cary NC
Lambert; Dennis Michael Cary NC
Petteway; Stephen Robert Cary NC

US-CL-CURRENT: 435/5; 424/147.1, 424/206.1, 424/230.1, 530/324, 530/389.4

ABSTRACT:

The present invention relates to peptides which exhibit potent anti-retroviral activity. The peptides of the invention comprise DP178 (SEQ ID:1) peptide corresponding to amino acids 638 to 673 of the HIV-1.sub.LAI gp41 protein, and fragments, analogs and homologs of DP178. The invention further relates to the uses of such peptides as inhibitory of human and non-human retroviral, especially HIV, transmission to uninfected cells.

5 Claims, 52 Drawing figures Exemplary Claim Number: 1 Number of Drawing Sheets: 83

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Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments

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29. Document ID: US 6060065 A

L7: Entry 29 of 46

File: USPT

May 9, 2000

US-PAT-NO: 6060065

DOCUMENT-IDENTIFIER: US 6060065 A

TITLE: Compositions for inhibition of membrane fusion-associated events, including influenza

virus transmission

DATE-ISSUED: May 9, 2000

INVENTOR-INFORMATION:

NAME CITY STATE ZIP CODE COUNTRY

Barney; Shawn O'Lin Cary NC
Lambert; Dennis Michael Cary NC
Petteway; Stephen Robert Cary NC

US-CL-CURRENT: 424/209.1; 424/186.1, 424/192.1, 424/206.1, 530/300, 530/324, 530/325, 530/326, 530/327, 530/328, 530/329, 530/330

ABSTRACT:

The present invention relates to viral peptides referred to as "DP107- and DP178-like" peptides. Specifically, the invention relates to isolated influenza A DP107- and DP178-like peptides which are identified by sequence search motif algorithms. The peptides of the invention exhibit antiviral activity believed to result from inhibition of viral induced fusogenic events.

5 Claims, 84 Drawing figures

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Exemplary Claim Number: 1 Number of Drawing Sheets: 83

Full Title Citation Front Review Classification Date Reference Sequences Attachments

KWIC Draw, Desc Image

30. Document ID: US 6054265 A

L7: Entry 30 of 46 File: USPT Apr 25, 2000

US-PAT-NO: 6054265

DOCUMENT-IDENTIFIER: US 6054265 A

TITLE: Screening assays for compounds that inhibit membrane fusion-associated events

DATE-ISSUED: April 25, 2000

INVENTOR - INFORMATION:

NAME CITY STATE ZIP CODE COUNTRY

Barney; Shawn O'Lin Cary NC
Lambert; Dennis Michael Cary NC
Petteway, Jr.; Stephen Robert Cary NC

US-CL-CURRENT: 435/5; 435/7.2

ABSTRACT:

The present invention relates to peptides which exhibit potent anti-retroviral activity. The peptides of the invention comprise DP178 (SEQ ID:1) peptide corresponding to amino acids 638 to 673 of the HIV-1.sub.LAI gp41 protein, and fragments, analogs and homologs of DP178. The invention further relates to the uses of such peptides as inhibitory of human and non-human retroviral, especially HIV, transmission to uninfected cells.

1 Claims, 83 Drawing figures Exemplary Claim Number: 1 Number of Drawing Sheets: 83

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments

KWIC | Draw, Desc | Image

31. Document ID: US 6048514 A

L7: Entry 31 of 46 File: USPT Apr 11, 2000

US-PAT-NO: 6048514

DOCUMENT-IDENTIFIER: US 6048514 A

TITLE: Amylin activity assays

DATE-ISSUED: April 11, 2000

INVENTOR-INFORMATION:

NAME CITY STATE ZIP CODE COUNTRY

Young; Andrew A. San Diego CA
Cooper; Garth J. S. Solana Beach CA
Rink; Timothy J. La Jolla CA

US-CL-CURRENT: 424/9.2; 514/12, 514/21, 514/866, 514/884

ABSTRACT:

Novel methods for use in identifying or assaying compounds which can simulate the ability of

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amylin to cause hyperlactemia and hyperglycemia in in vivo biological models, or for use in evaluating the potency of compounds known or suspected to simulate these actions of amylin, which involve introducing test samples into in vivo test systems and determining the presence or amount of a rise in lactate, or determining the presence or amount of a rise in lactate and a rise in glucose, following test sample administration.

12 Claims, 24 Drawing figures Exemplary Claim Number: 1 Number of Drawing Sheets: 15

Full Title Citation Front Review Classification Date Reference Sequences Attachments

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32. Document ID: US 6020139 A

L7: Entry 32 of 46

File: USPT

Feb 1, 2000

US-PAT-NO: 6020139

DOCUMENT-IDENTIFIER: US 6020139 A

TITLE: S-adenosyl methionine regulation of metabolic pathways and its use in diagnosis and

therapy

DATE-ISSUED: February 1, 2000

INVENTOR-INFORMATION:

NAME CITY STATE ZIP CODE COUNTRY

Schwartz; Dennis E. Redmond WA
Vermeulen; Nicolaas M. J. Woodinville WA
O'Day; Christine L. Mountlake Terrace WA

US-CL-CURRENT: 435/7.1; 435/192, 514/556

ABSTRACT:

A new paradigm of disease centers around the metabolic pathways of S-adenosyl-L-methionine (SAM), the intermediates of these pathways and other metabolic pathways influenced by the SAM pathways. Methods are provided to analyze and modulate SAM pathways associated with a disease or condition. Such methods permit identification and utilization of diagnostic and therapeutic protocols and agents for such disease states and conditions.

18 Claims, 12 Drawing figures Exemplary Claim Number: 1 Number of Drawing Sheets: 12

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Full	Title	Citation	Front	Review	Classification	Date	Reference l	Sequences	Attachments

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33. Document ID: US 6017536 A

L7: Entry 33 of 46

File: USPT

Jan 25, 2000

US-PAT-NO: 6017536

DOCUMENT-IDENTIFIER: US 6017536 A

TITLE: Simian immunodeficiency virus peptides with antifusogenic and antiviral activities

DATE-ISSUED: January 25, 2000

INVENTOR-INFORMATION:

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COUNTRY

ZIP CODE

NAME CITY STATE
Barney; Shawn O'Lin Cary NC
Lambert; Dennis Michael Cary NC
Petteway; Stephen Robert Cary NC
Langlois; Alphonse J. Durham NC

US-CL-CURRENT: 424/188.1; 424/208.1, 530/300, 530/324, 530/325, 530/326

ABSTRACT:

The present invention relates to peptides which exhibit antifusogenic and antiviral activities. The peptides of the invention consist of a 16 to 39 amino acid region of a simian immunodeficiency virus (SIV) protein. These regions were identified through computer algorithms capable of recognizing the ALLMOTI5, 107.times.178.times.4, or PLZIP amino acid motifs. These motifs are associated with the antifusogenic and antiviral activities of the claimed peptides.

28 Claims, 50 Drawing figures Exemplary Claim Number: 1 Number of Drawing Sheets: 62

Full	Title Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments	KWAC DI	aw. Des	c Image
	34. Docum	ment I	D: US	6013263 A							
L7: E	Entry 34 of	46				File	e: USPT		Jan	11,	2000

US-PAT-NO: 6013263

DOCUMENT-IDENTIFIER: US 6013263 A

TITLE: Measles virus peptides with antifusogenic and antiviral activities

DATE-ISSUED: January 11, 2000

INVENTOR - INFORMATION:

NAME CITY STATE ZIP CODE COUNTRY
Barney; Shawn O'Lin Cary NC
Lambert; Dennis Michael Cary NC
Petteway; Stephen Robert Cary NC

US-CL-CURRENT: 424/212.1; 424/184.1, 424/186.1, 530/300, 530/324, 530/325, 530/326

ABSTRACT:

The present invention relates to peptides which exhibit potent anti-retroviral activity. The peptides of the invention comprise DP178 (SEQ ID:1) peptide corresponding to amino acids 638 to 673 of the HIV-1.sub.LAI gp41 protein, and fragments, analogs and homologs of DP178. The invention further relates to the uses of such peptides as inhibitory of human and non-human retroviral, especially HIV, transmission to uninfected cells.

38 Claims, 52 Drawing figures Exemplary Claim Number: 1 Number of Drawing Sheets: 83

Full Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments	KUMC Draw Desc Im-
Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments	KVVIC Drawl Desc Im

L7: Entry 35 of 46 File: USPT Aug 17, 1999

US-PAT-NO: 5939284

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